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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1	AR247677	AR2274677	Sequence 1 from patent AR274677	19 bp	DNA	linear	PAT 10-APR-2003
LOCUS				US 6506600.				
DEFINITION								
ACCESSION								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								

Unknown. Unknown. Unclassified. 1 (bases 1 to 19)
 Hermonat, P.L., Mane, M. and Liu, Y.
 Secreting products from skin by adeno-associated virus (AAV) gene
 transfer
 Patent: US 6506600-A 1 14-JAN-2003;

Pred. No. is the number of results predicted by chance to have a

KEYWORDS	JP 1999243959-A/5.	ORIGIN	Query Match 52.6%; Score 10; DB 6; Length 19;
SOURCE	Homo sapiens (human)		Best Local Similarity 52.6%; Pred. No. 2.e+04;
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 19)		Mismatches 9; Indels 0; Gaps 0;
REFERENCE		Qy	1 CCAATNNNNNNNNCCAGC 19
AUTHORS	Hideo, Y., Hideki, Y. and Takashi, Y.	Db	1 CCAATGGGGCTCCACG 19
TITLE	Endoplasmic reticulum stress-response regulatory element	RESULT 7	19 bp
JOURNAL	PATENT: JP 1999243959-A 5 14-SEP-1999; HSP RESEARCH INST INC	LOCUS	DNA linear
COMMENT	OS Homo sapiens (human)	E28803	PAT 18-JUN-2001
	PN JP 1999243959-A/5	E28803	Endoplasmic reticulum stress-response regulatory element.
	PD 14-SEP-1999	E28803	
	PF 04-MAR-1998 JP 1998052453	E28803	
PI	HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA	DEFINITION	
PC	C12N15/09 A61K5/74, A61K38/00, A61K48/00, C12N15/00,	VERSION	
PC	A61K5/02	KEYWORDS	
CC	Strandedness: Double;	SOURCE	
CC	Topology: Linear;	ORGANISM	Rattus sp.
PH	Key		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
PT	enhancer 1..19.	REFERENCE	1 (bases 1 to 19)
	Location/Qualifiers	AUTHORS	Hideo, Y., Hideki, Y. and Takashi, Y.
	1..19	TITLE	Endoplasmic reticulum stress-response regulatory element
FEATURES	/organism="Homo sapiens"	JOURNAL	PATENT: JP 1999243959-A 7 14-SEP-1999; HSP RESEARCH INST INC
SOURCE	/mol_type="genomic DNA"	COMMENT	OS Rattus sp. (rat)
	/db_xref="taxon:9606"		PN JP 1999243959-A/7
BASE COUNT	3 a 9 c 5 g 2 t		PD 14-SEP-1999
ORIGIN	Query Match 52.6%; Score 10; DB 6; Length 19;		CC 04-MAR-1998 JP 1998052453
	Best Local Similarity 52.6%; Pred. No. 2.7e+04;		PR HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
	Mismatches 10; Conservative 0; Gaps 0;		PC C12N15/09, A61K35/74, A61K38/00, A61K48/00, C12N15/00,
Qy	1 CCAATNNNNNNNNCCAGC 19		A61K37/02
Db	1 CCAATGGGGCTCCACG 19		CC Strandedness: Double;
RESULT 6	19 bp		CC Topology: Linear;
LOCUS	E28802		FH Key Location/Qualifiers
DEFINITION	Endoplasmic reticulum stress-response regulatory element.		FT enhancer 1..19.
ACCESSION	E28802		LOCATION/QUALIFIERS
VERSION	E28802.1 GI:13020856		1..19
KEYWORDS	JP 1999243959-A/6.		/organism="Rattus sp."
SOURCE	Mus sp.		/mol_type="genomic DNA"
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 19)		/db_xref="taxon:10118"
REFERENCE	Hideo, Y., Hideki, Y. and Takashi, Y.		
AUTHORS	Endoplasmic reticulum stress-response regulatory element		
TITLE	PATENT: JP 1999243959-A 6 14-SEP-1999; HSP RESEARCH INST INC		
JOURNAL	Mus sp. (mouse)		
COMMENT	PN JP 1999243959-A/6		
	PD 14-SEP-1999		
	PF 04-MAR-1998 JP 1998052453		
FEATURES	1..19		
SOURCE	/organism="Mus sp."		
BASE COUNT	4 a 8 c 5 g 2 t		
ORIGIN	Query Match 52.6%; Score 10; DB 6; Length 19;	RESULT 8	19 bp
	Best Local Similarity 52.6%; Pred. No. 2.7e+04;	LOCUS	DNA linear
	Mismatches 10; Conservative 0; Gaps 0;	DEFINITION	PAT 18-JUN-2001
Qy	1 CCAATNNNNNNNNCCAGC 19	ACCESSION	Endoplasmic reticulum stress-response regulatory element.
Db	1 CCAATGGGGCTCCACG 19	VERSION	E28804
RESULT 8	19 bp	KEYWORDS	E28804.1 GI:13020858
LOCUS	E28804	SOURCE	JP 1999243959-A/8
DEFINITION	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 19)	ORGANISM	Homo sapiens (human)
ACCESSION	E28804		
VERSION	E28804.1 GI:13020858		
KEYWORDS	Hideo, Y., Hideki, Y. and Takashi, Y.		
SOURCE	Endoplasmic reticulum stress-response regulatory element		
ORGANISM	PATENT: JP 1999243959-A 8 14-SEP-1999; HSP RESEARCH INST INC		
REFERENCE	1..19		
AUTHORS	/organism="Mus sp."		
TITLE	/mol_type="genomic DNA"		
JOURNAL	/db_xref="taxon:10095"		
BASE COUNT	4 a 8 c 5 g 2 t		

	Mus sp.	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus
	1. 19	REFERENCE	1 (bases 1 to 19)
FEATURES	Key enhancer	AUTHORS	Hideo,Y., Hideki,Y. and Takashi,Y.
source	Location/Qualifiers	TITLE	Endoplasmic reticulum stress-response regulatory element
	1. .19	JOURNAL	Patent: JP 1992A3959-A 13-SEP-1993;
	/organism="Gallus sp."	COMMENT	HSP RESEARCH INST INC
	/mol_type="genomic DNA"	OS	Mus sp. (mouse)
BASE COUNT	4 a 9 c 5 g 1 t	PN	JP 1992A3959-A/13
ORIGIN		PD	04-SEP-1999
		PR	04-MAR-1998 JP 199805453
Query Match	52.6%; Score 10; DB 6; Length 19;	PI	HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
Best Local Similarity	52.6%; Pred. No. 2.7e+04;	PC	C12N15/09_A61K35/76_A61K38/00_A61K48/00_C12N15/00,
Matches 10;	0; Mismatches 9; Indels 0; Gaps 0;	PC	A61K37/02
Conservative		CC	Strandedness: Double;
		FH	Topology: Linear;
		FT	Key enhancer Location/Qualifiers
			1. .19
Qy	1 CCAATNNNNNNNNCCACG 19	FEATURES	Source
		1. .19	/organism="Mus sp."
Db	1 CCATCGAGGCCACG 19		/mol_type="genomic DNA"
			/db_xref="taxon:10095"
RESULT 12	E28808	BASE COUNT	5 a 6 c 6 9 2 t
LOCUS	Endoplasmic reticulum stress-response regulatory element.	FEATURES	Source
DEFINITION	PAT 18-JUN-2001	Query Match	52.6%; Score 10; DB 6; Length 19;
ACCESSION	E28808	Best Local Similarity	52.6%; Pred. No. 2.7e+04;
	E28808.1 GI:13020862	Matches	0; Mismatches 9; Indels 0; Gaps 0;
KEYWORDS	JP 1992A3959-A/12.	Qy	1 CCAATNNNNNNNNCCACG 19
SOURCE	Homo sapiens (human)	Db	1 CCATGGGTGACCCACG 19
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19)	RESULT 14	LINEAR
		LOCUS	E44202
COMMENT	Homo sapiens (human)	DEFINITION	Endoplasmic reticulum stress transcription factor.
OS	JP 1992A3959-A/12	ACCESSION	E44202
PN	14-SEP-1999	VERSION	E44202_1 GI:16633455
PD		KEYWORDS	JP 2001054391-A1.
PR	04-MAR-1998 JP 1998052453	SOURCE	Synthetic construct
		ORGANISM	Artificial sequences.
		REFERENCE	Haji,K. Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
REFERENCE		AUTHORS	
AUTHORS	Hideo,Y., Hideki,Y. and Takashi,Y.	TITLE	Endoplasmic reticulum stress transcription factor
TITLE	Endoplasmic reticulum stress-response regulatory element	JOURNAL	Patent: JP 2001054391-A 1 27-FEB-2001;
JOURNAL	Patent: JP 1992A3959-A 12 14-SEP-1999;	COMMENT	HSP RESEARCH INST INC
COMMENT	HSP RESEARCH INST INC	OS	Artificial Sequence
OS		PN	JP 2001054391-A/1
PN		PD	27-FEB-2001
PD		PP	11-NOV-1999 JP 1999321743
PR		PI	KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
		PC	C12N15/09_C12P21/02// (C12N15/09_C12R1:91), C12N15/00_C12R1:91)
		CC	
		FH	Key source
		FT	Location/Qualifiers
			1. .19
FEATURES	Key enhancer	FEATURES	Source
source	Location/Qualifiers	1. .19	/organism="Artificial Sequence".
	1. .19		
	/organism="Homo sapiens"		1. .19
	/mol_type="genomic DNA"		/organism="synthetic construct"
	/db_xref="taxon:32630"		/mol_type="genomic DNA"
BASE COUNT	5 a 6 c 5 g 3 t		
ORIGIN			
RESULT 13	E28809	FEATURES	Source
LOCUS	Endoplasmic reticulum stress-response regulatory element.	Query Match	52.6%; Score 10; DB 6; Length 19;
DEFINITION	PAT 18-JUN-2001	Best Local Similarity	52.6%; Pred. No. 2.7e+04;
ACCESSION	E28809	Matches	0; Mismatches 9; Indels 0; Gaps 0;
VERSION	E28809.1 GI:13020863	Qy	1 CCAATNNNNNNNNCCACG 19
KEYWORDS	JP 1992A3959-A/13.	Db	1 CCAATGGTGTGACCCACG 19
SOURCE	Mus sp.	RESULT	Mus sp.
		BASE COUNT	3 a -5 c 1 g 1 t 9 others

Query Match Score 10; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.7e+04;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 1 CCAATNNNNNNNNCCACG 19

RESULT 15

B44206 E44206 19 bp DNA linear PAT 31-JAN-2002
 LOCUS Endoplasmic reticulum stress transcription factor.
 DEFINITION E44206
 ACCESSION E44206_1 GI:19633459
 VERSION JP 2001054391-A/5.
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Haji, K., Yoshida, H., Mori, K., Yanagi, H. and Yura, T.
 TITLE Endoplasmic reticulum stress transcription factor
 JOURNAL Patent: JP 2001054391-A 5 27-FEB-2001;
 HSP RESEARCH INST INC
 COMMENT OS Homo sapiens (human)
 PN JP 2001054391-A/5
 PD 27-FEB-2001
 PF 11-NOV-1999 JP 1999321743
 PR
 PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
 PC C12N15/09, C12P21/02 // (C12N15/09, C12R1:91), C12N15/00, (C12N15/00, PC
 C12R1:91)
 CC
 FH Key
 FT source
 FT source Location/Qualifiers
 FEATURES source 1..19
 /organism='Homo sapiens (human)'.
 BASE COUNT 3 a 9 c 5 g 2 t
 ORIGIN
 Query Match Score 10; DB 6; Length 19;
 Best Local Similarity 52.6%; Pred. No. 2.7e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 1 CCAATGGGGCTCCACG 19

Search completed: December 4, 2003, 09:21:23
 Job time : 1501 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 07:47:59 ; Search time 261 Seconds
 (without alignments)
 196.511 Million cell updates/sec

Title: US-09-606-804-1
 Perfect score: 19
 Sequence: 1 ccaatnnnnnnccacg 19

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
 Listing first 45 summaries
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 2: /SIDS1/gcgdata/geneseq/geneseq/geneseq-emb1/NA1981.DAT;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	10	52.6	19	20	AZ225631 Endoplasmic reticulum
2	10	52.6	19	20	AZ225632 Endoplasmic reticulum
3	10	52.6	19	20	AZ225633 Endoplasmic reticulum
4	10	52.6	19	20	AZ225634 Endoplasmic reticulum
5	10	52.6	19	20	AZ225635 Endoplasmic reticulum
6	10	52.6	19	20	AZ225636 Endoplasmic reticulum
7	10	52.6	19	20	AZ225637 Endoplasmic reticulum
8	10	52.6	19	20	AZ225638 Endoplasmic reticulum

Homo sapiens.

OS

XX

PN

XX

PD

XX

PP

XX

PR

XX

PA

XX

DR

XX

PT

PT

PT

RESULT 1
 AA225631 standard; DNA; 19 BP.

XX
 38 10 52.6 112 24 AB141923
 39 10 52.6 122 20 AA225660
 40 10 52.6 122 21 AAA28566
 41 10 52.6 123 24 AB180984
 42 10 52.6 126 21 AAAT1906
 43 10 52.6 127 24 ABL41924
 44 10 52.6 143 21 AAA71907
 C 45 10 52.6 145 22 AAF67488

ALIGNMENTS

XX
 23-DEC-1999 (first entry)
 ID AA225631 standard; DNA; 19 BP.
 XX
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:1.
 KW Endoplasmic reticulum; ER; stress competence; control element;
 KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX
 Homo sapiens.

XX
 JP11243959-A.XX
 14-SEP-1999.XX
 PN 98JP-0052453.XX
 PD 04-MAR-1998;XX
 PR 04-MAR-1998;XX
 PA (HSPK-) HSP KENKYUSHO KK.XX
 XX WPI; 1999-603708/52.XX
 PT New control element for stress competence of endoplasmic reticulum -

PT useful for inhibition of growth and induction of apoptosis in cancer

PT cells

XX	PS	Claim 1; Page 10; 25pp; Japanese.
XX	CC	The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation.
XX	SQ	Sequence 19 BP; 3 A; 5 C; 5 G; 2 T; 0 other;
XX	Qy	Query Match 52.6%; Score 10; DB 20; Length 19; Best Local Similarity 52.6%; Pred. No. 1.8e+03; Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX	Db	1 CCAATNNNNNNNNNNCCACG 19 1 CCAATGGGGCCTCCACG 19
XX	RESULT 3	AAZ25633 standard; DNA; 19 BP.
XX	ID	AAZ25633
XX	AC	AAZ25633;
XX	DT	23-DEC-1999 (first entry)
XX	DS	Endoplasmic reticulum stress competence control element SEQ ID NO:6.
XX	KW	Endoplasmic reticulum; ER; Stress competence; control element; inhibition; growth; apoptosis; cancer; autoimmune disease; cystic fibrosis; ds.
XX	KW	XX
XX	XX	XX
XX	XX	XX
XX	XX	XX
XX	OS	Mus sp.
XX	PN	JP11243959-A.
XX	PD	14-SEP-1999.
XX	PP	04-MAR-1998; 98JP-0052453.
XX	PR	04-MAR-1998; 98JP-0052453.
XX	PA	(HSPK-) HSP KENKYUSHO KK.
XX	PA	WPI; 1999-603708/52.
XX	PT	New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer cells
XX	PT	XX
XX	PS	Example 1; Fig 3; 25pp; Japanese.
XX	CC	The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in an example from the present invention.
XX	SQ	Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
XX	Qy	Query Match 52.6%; Score 10; DB 20; Length 19; Best Local Similarity 52.6%; Pred. No. 1.8e+03; Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX	Db	1 CCAATNNNNNNNNNNCCACG 19 1 CCAATGGGGCCTCCACG 19
XX	RESULT 4	AAZ25634

ID AAZ25634 standard; DNA; 19 BP.
 XX
 AC AAZ25634;
 XX
 DT 23-DEC-1999 (first entry)
 XX
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:7.
 XX
 KW Endoplasmic reticulum; ER; stress competence; control element;
 KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX
 OS Rattus sp.
 XX
 PN JP11243959-A.
 XX
 PD 14-SEP-1999.
 XX
 PF 04-MAR-1998; 98JP-0052453.
 XX
 PR 04-MAR-1998; 98JP-0052453.
 XX
 PA (HSPK-) HSP KENKYUSHO KK.
 XX
 DR WPI; 1999-603708/52.
 XX
 PT New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer
 PT cells.
 XX
 PS Example 1; Fig 3; 25pp; Japanese.

XX
 CC The present invention specifically claims an element shown by: (A) a
 CC 19 bp base sequence, CCAATNNNN NNNNCACG (ERSE); or (B) a modified base
 CC sequence having replaced 1-3 bases with the other base(s), which induces
 CC transcription with stress on endoplasmic reticulum used for stress
 CC competence of endoplasmic reticulum. Also described are: (1) a DNA
 CC having transcription inducing activity with stress on endoplasmic
 CC reticulum containing the above mentioned element, optionally further
 CC containing a promoter DNA; and (2) a vector containing the element
 CC optionally with the DNA. The element can be used for the inhibition of
 CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
 CC antibody formation. AAZ25632 to AAZ25657 represent elements used in
 CC an example from the present invention.

SQ Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
 SQ Query Match 52.6%; Score 10; DB 20; Length 19;
 SQ Best Local Similarity 52.6%; Pred. No. 1.8E+03;
 SQ Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 SQ Qy 1 CCAATNNNNNNNNNNCACG 19
 SQ Db 1 CCAATGGCGCCGACACG 19
 SQ RESULT 6
 SQ AAZ25636
 ID AAZ25636 standard; DNA; 19 BP.
 XX
 AC AAZ25636;
 XX
 DT 23-DEC-1999 (first entry)
 XX
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:9.
 XX
 KW Endoplasmic reticulum; ER; stress competence; control element;
 KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX
 OS Gallus sp.
 XX
 PN JP11243959-A.
 XX
 AC AAZ25635;
 XX
 DT 23-DEC-1999 (first entry)
 XX
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:8.
 XX
 KW Endoplasmic reticulum; ER; stress competence; control element;
 KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX
 OS Homo sapiens.

XX
 PT New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer

PT Example 1; Fig 3; 25pp; Japanese.
 XX
 PS

The present invention specifically claims an element shown by: (A) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in an example from the present invention.

XX Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;

SQ Query Match 52.6%; Score 10; DB 20; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNCCACG 19

Db 1 CCAATGGAAAGGACACCG 19

RESULT 8

AAZ25638

ID AAZ25638 standard; DNA; 19 BP.

XX AAZ25638;

XX DT 23-DEC-1999 (first entry)

XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:11.

XX KW Endoplasmic reticulum; ER; stress competence; control element;

XX KW Inhibition; growth; apoptosis; cancer; autoimmune disease;

XX KW Cystic fibrosis; ds.

XX OS Gallus sp.

XX PN JP11243959-A.

XX PD 14-SEP-1999.

XX PR 04-MAR-1998; 98JP-0052453.

XX PR 04-MAR-1998; 98JP-0052453.

XX PA (HSPK-) HSP KENKYUSHO KK.

XX DR WPI; 1999-603708/52.

XX PT New control element for stress competence of endoplasmic reticulum -

XX PT useful for inhibition of growth and induction of apoptosis in cancer

XX PT cells

XX PS Example 1; Fig 3; 25pp; Japanese.

XX The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNN NNNNCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in an example from the present invention.

XX Sequence 19 BP; 4 A; 9 C; 5 G; 1 T; 0 other;

SQ Query Match 52.6%; Score 10; DB 20; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNCCACG 19

Db 1 CCAATGAGGGCAGCAG 19

RESULT 9
 AA225639 standard; DNA; 19 BP.
 XX
 AC AA225639;
 XX
 DT 23-DEC-1999 (first entry)
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:12.
 DE XX
 KW Endoplasmic reticulum; ER; stress competence; control element;
 inhibition; growth; apoptosis; cancer; autoimmune disease;
 cystic fibrosis; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP11243959-A.
 XX
 PD 14-SEP-1999.
 XX
 PF 04-MAR-1998; 98JP-0052453.
 XX
 PA (HSPK-) HSP KENKYUSHO KK.
 XX
 DR WPI; 1999-603708/52.
 XX
 PT New control element for stress competence of endoplasmic reticulum -
 useful for inhibition of growth and induction of apoptosis in cancer
 cells.
 XX
 PS Example 1; Fig 3; 25pp; Japanese.

XX
 CC The present invention specifically claims an element shown by: (A) a
 19 bp base sequence, CCAATNNNN NNNNCCACG (ERSE); or (B) a modified base
 sequence having replaced 1-3 bases with the other base(s), which induces
 transcription with stress on endoplasmic reticulum used for stress
 competence of endoplasmic reticulum. Also described are: (1) a DNA
 having transcription inducing activity with stress on endoplasmic
 reticulum containing the above mentioned element, optionally further
 containing a Promoter DNA; and (2) a vector containing the element
 optionally with the DNA. The element can be used for the inhibition of
 growth and induction of apoptosis of cancer cells, and improvement of
 symptoms of autoimmune diseases and cystic fibrosis by inhibition of
 autoantibody formation. AA225632 to AA225637 represent elements used in
 an example from the present invention.

XX
 CC Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;

CC
 CC Query Match 52.6%; Score 10; DB 20; Length 19;
 CC Best Local Similarity 52.6%; Pred. No. 1.8e+03;
 CC Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

CC
 CC Qy 1 CCAATNNNNNNNNNCACG 19
 CC Db 1 CCAATGAGGTGACACAGC 19

CC RESULT 11
 CC AAA28570
 CC ID AA228570 standard; DNA; 19 BP.
 CC XX
 CC AC AAA28570;
 CC DT 29-AUG-2000 (first entry)
 CC DE GRP78 promoter ERSB1-like sequence.
 CC XX
 CC KW Endoplasmic reticulum; stress; ER; transcription factor;
 CC transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 CC prophyaxis; cancer; arteriosclerosis; ischaemia; wound healing;
 CC cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
 CC gene expression; GRP; glucose regulated protein; promoter; ss.
 CC XX
 CC Homo sapiens.

CC OS WO20029429-A2.

CC PN
 CC XX
 CC DT 23-DEC-1999 (first entry)
 CC XX
 CC DE Endoplasmic reticulum stress competence control element SEQ ID NO:13.
 CC XX
 CC KW Endoplasmic reticulum; ER; stress competence; control element;
 CC inhibition; growth; apoptosis; cancer; autoimmune disease;
 CC cystic fibrosis; ds.
 CC XX
 CC PR 13-NOV-1998;
 CC PR 99WO-JP06305.
 CC XX
 CC PR 09-JUN-1999;
 CC PR 98JP-0324227.
 CC XX
 CC PR 0163112.

XX An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of an endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP78 contains an ERSE like sequence.

XX Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;

SQ Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
| | || |
Db 1 CCAATGGAGCCCTCCACG 19

RESULT 14
AAA28573

ID AAA8573 standard; DNA; 19 BP.
XX AC AAA28573;
XX DE 29-AUG-2000 (first entry)
DE GRR94 promoter ERSE1-like sequence.

XX Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; KW cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken; KW gene expression; GRP; glucose regulated protein; promoter; ss. OS Gallus domesticus.
XX PN WO20002429-A2.
XX PR 13-NOV-1998; 988P-0324227.
XX PD 25-MAY-2000.
XX PA (HSPR-) HSP RES INST INC.
XX PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX DR 12-NOV-1999; 99W0-JP06305.
XX PR 09-JUN-1999; 99JP-0163112.
XX PA (HSPR-) HSP RES INST INC.
XX PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX DR 2000-387736/33.
XX PT New endoplasmic reticulum stress transcription factor (known as bZIP)
PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers
XX Example 1: Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (known as bZIP)
CC capable of regulating transcription inducing activity exhibited by an
CC element (ERSE) can be used in a method for controlling expression of
CC an endoplasmic reticulum chaperone. The method comprises expressing
CC bZIP. The method can be used for expression of foreign protein by
CC positively regulating expression of an endoplasmic reticulum
CC chaperone gene. bZIP is useful for controlling the expression of
CC endoplasmic reticulum chaperone either positively or negatively in
CC cells and therefore is useful for treatment or prophylaxis of
CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
CC wounds and ulcers. bZIP also maintains the correct conformation of

XX positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of an endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP94 contains an ERSE like sequence.

XX Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;

SQ Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
| | || |
Db 1 CCAATGGCGCGCACACG 19

RESULT 15
AAA28574

ID AAA28574 standard; DNA; 19 BP.

XX XX AC AAA28574;
XX DE 29-AUG-2000 (first entry)
DE GRP94 promoter ERSE1-like sequence.

XX KW Endoplasmic reticulum; stress; ER; transcription factor;
KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
KW cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken;
KW gene expression; GRP; glucose regulated protein; promoter; ss.

OS XX PN WO20002429-A2.
XX PR 13-NOV-1998; 988P-0324227.
XX PD 09-JUN-1999; 99JP-0163112.
XX PA (HSPR-) HSP RES INST INC.

XX PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

XX DR 2000-387736/33.

XX PT New endoplasmic reticulum stress transcription factor (known as bZIP)

PT for controlling expression of endoplasmic reticulum chaperone, useful
PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT diseases, wounds and ulcers

XX PS Example 1: Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (known as bZIP)

CC capable of regulating transcription inducing activity exhibited by an

CC element (ERSE) can be used in a method for controlling expression of

CC an endoplasmic reticulum chaperone. The method comprises expressing

CC bZIP. The method can be used for expression of foreign protein by

CC positively regulating expression of an endoplasmic reticulum

CC chaperone gene. bZIP is useful for controlling the expression of

CC endoplasmic reticulum chaperone either positively or negatively in

CC cells and therefore is useful for treatment or prophylaxis of

CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,

CC wounds and ulcers. bZIP also maintains the correct conformation of

the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP94 contains an ERSSE like sequence.

XX
SQ Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
| || |
Db 1 CCAATGGAGCACCACG 19

Search completed: December 4, 2003, 08:56:09
Job time : 262 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 08:47:17 ; Search time 75 Seconds
(without alignments)
111.817 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19

Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*

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6: /cgn2_6/podata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	52.6	19	4	US-09-813-937-1
C 2	10	52.6	205	4	US-09-313-294A-1696
C 3	10	52.6	261	4	US-09-389-681-206
4	10	52.6	261	4	US-09-620-405B-206
5	10	52.6	261	4	US-09-339-338-206
6	10	52.6	261	4	US-09-433-826B-206
7	10	52.6	261	4	US-09-604-287A-206
C 8	10	52.6	270	4	US-09-313-294A-890
C 9	10	52.6	272	1	US-08-278-474-36
10	10	52.6	272	3	US-08-756-849-36
11	10	52.6	282	4	US-09-252-991A-987
12	10	52.6	285	4	US-09-252-991A-60
C 13	10	52.6	296	2	US-08-716-942-20
C 14	10	52.6	300	4	US-09-313-337A-20
C 15	10	52.6	300	4	US-09-313-294A-7348
C 16	10	52.6	300	4	US-09-404-879A-372
C 17	10	52.6	387	3	US-08-804-372A-23
C 18	10	52.6	392	4	US-09-404-879A-372
C 19	10	52.6	399	6	US-09-404-879A-372
C 20	10	52.6	421	6	5196523-23
C 21	10	52.6	424	1	5196523-22
C 22	10	52.6	432	4	US-08-609-657-15
C 23	10	52.6	457	4	US-09-252-991A-9959
C 24	10	52.6	457	4	US-09-702-705-861
C 25	10	52.6	467	3	US-09-257-584-8
C 26	10	52.6	511	4	US-09-702-705-1138
C 27	10	52.6	511	4	US-09-736-457-1138

ALIGNMENTS

RESULT 1

US-09-813-937-1 ; Sequence 1, Application US/09813937 ; Patent No. 6506600 ; GENERAL INFORMATION: ; APPLICANT: HERMONAT, Paul L. ; INVENTOR: LIU, Yong ; TITLE OF INVENTION: SECRETING PRODUCTS FROM SKIN BY ADENO-ASSOCIATED VIRUS (AAV) GEN. FILE REFERENCE: 023533/0116 ; CURRENT APPLICATION NUMBER: US/09/883,937 ; PRIORITY APPLICATION NUMBER: US 60/191092 ; PRIORITY FILING DATE: 2000-03-22 ; NUMBER OF SEQ ID NOS: 4 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 1 ; LENGTH: 19 ; TYPE: DNA ; ORGANISM: Unknown ; FEATURE: OTHER INFORMATION: glucose response element ; FEATURE: NAME/KEY: misc_feature ; LOCATION: (6) (14) ; OTHER INFORMATION: "N" at positions 6 - 14 can be A, C, G or T ; US-09-813-937-1

Query Match 52.6%; Score 10; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ; Gaps 0;

Qy 1 CCATNNNNNNNNNNNCACG 19 Db 1 CCATNNNNNNNNNNNCACG 19

RESULT 2

US-09-313-29A-1696/c ; Sequence 1696, Application US/09313294A ; Patent No. 6476212 ; GENERAL INFORMATION: ; APPLICANT: Laligudi, Raghunath V. ; INVENTOR: Ito, Lauri Y. ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US ; CURRENT APPLICATION NUMBER: US/09/313,294A ; CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600
 SOFTWARE: PERL Program
 SEQ ID NO 1696
 LENGTH: 205
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID NO. 6476212 700551354H1
 US-09-313-294A-1696

Query Match 52.6%; Score 10; DB 4; Length 205;
 Best Local Similarity 52.6%; Pred. No. 5.2e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 122 CCAATCAGACAGACCCACG 104

RESULT 3
 US-09-389-681-206
 Sequence 206, Application US/09389681A
 Patent No. 6518237
 GENERAL INFORMATION:
 APPLICANT: Yuqiu, Jiang
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Heppler, William T.
 TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE: 10/21.470C3
 CURRENT FILING DATE: 1999-09-02
 NUMBER OF SEQ ID NOS: 463
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 206
 LENGTH: 261
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-389-681-206

Query Match 52.6%; Score 10; DB 4; Length 261;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 140 CCAATTCTCATCTCCACG 158

RESULT 4
 US-09-620-405B-206
 Sequence 206, Application US/09620405B
 Patent No. 652054
 GENERAL INFORMATION:
 APPLICANT: Jiang, Yuqiu
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Heppler, William T.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF BREAST CANCER
 FILE REFERENCE: 210121.470C8
 CURRENT APPLICATION NUMBER: US/09/620,405B
 CURRENT FILING DATE: 2000-07-20
 NUMBER OF SEQ ID NOS: 495
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 206
 LENGTH: 261
 TYPE: DNA
 ORGANISM: Homo sapiens

US-09-620-405B-206
 Query Match 52.6%; Score 10; DB 4; Length 261;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 140 CCAATTCTCATCTCCACG 158

RESULT 5
 US-09-338-206
 Sequence 206, Application US/09339338A
 Patent No. 6573168
 GENERAL INFORMATION:
 APPLICANT: Yugu, Jiang
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Xu, Jiangchun
 TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE: 210121.470C2
 CURRENT APPLICATION NUMBER: US/09/338A
 CURRENT FILING DATE: 1999-06-23
 NUMBER OF SEQ ID NOS: 315
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 206
 LENGTH: 261
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-338-206

Query Match 52.6%; Score 10; DB 4; Length 261;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 140 CCAATTCTCATCTCCACG 158

RESULT 6
 US-09-433-826B-206
 Sequence 206, Application US/09433826B
 Patent No. 6573973
 GENERAL INFORMATION:
 APPLICANT: Jiang, Yuqiu
 APPLICANT: Dillon, Davin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Xu, Jiangchun
 TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
 FILE REFERENCE: 210121.470C4
 CURRENT APPLICATION NUMBER: US/09/433,826B
 CURRENT FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 474
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 206
 LENGTH: 261
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-433-826B-206

Query Match 52.6%; Score 10; DB 4; Length 261;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 140 CCAATTCTCATCTCCACG 158

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RESULT 7
US-09-604-287A-206
; Sequence 206, Application US/09604287A
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Repler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121..470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-206

Query Match      52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy          1 CCAATNNNNNNNNCCACG 19
                           ||||| | | | | |
Db          140 CCAATTCTTCATCTCCACG 158

RESULT 8
US-09-313-294A-890/C
; Sequence 890, Application US/09313294A
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL program
SEQ ID NO 890
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700550018H1
NAME/KEY: unsure
LOCATION: 213-215, 218-221, 232-233, 239-240, 242, 249, 251, 253, 255
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-890

Query Match      52.6%; Score 10; DB 4; Length 270;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy          1 CCAATNNNNNNNNCCACG 19
                           ||||| | | | | |
Db          121 CCATCAGACAGACGCCACG 103

RESULT 9
US-08-248-474-36
Sequence 36, Application US/08248474
Patent No. 5612471

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SOFTWARE: PatentIn Release #1.0, Version #1.1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/756,849
 FILING DATE: 26-NOV-1996
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,474
 FILING DATE: 25-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 023070-0551510US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEX/FAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 272 base pairs
 TYPE: nucleic acid
 STRANDBNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: /standard_name= "DB# 155"
 US-08-756-849-36

RESULT 11
 Query Match 52.6%; Score 10; DB 3; Length 272;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 97 CCAATATTATTACACCG 115

RESULT 12
 Query Match 52.6%; Score 10; DB 4; Length 282;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 49 CCAATGTGTACCCCCACG 67

RESULT 13
 Query Match 52.6%; Score 10; DB 4; Length 285;
 Best Local Similarity 52.6%; Pred. No. 5.5e+02; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 224 CCAATGACCGAATAACACG 242

Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIORITY APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 60
 LENGTH: 285
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-60

Query Match 52.6%; Score 10; DB 4; Length 285;
 Best Local Similarity 52.6%; Pred. No. 5.5e+02; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 224 CCAATGACCGAATAACACG 242

RESULT 13
 US-08-716-942-20/C
 Sequence 20, Application US/08716942
 Patent No. 5843491
 GENERAL INFORMATION:
 APPLICANT: Terragen Diversity Inc.
 Radomski, Christopher C. A.
 Seow, Kah Tong
 Warren, R. Antony J.
 APPPLICANT: Yap, Wai Ho
 TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENES
 SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND
 COMPOSITIONS OBTAINED THEREBY
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Oppedahl & Larson
 STREET: 1992 Commerce Street, Suite 309
 CITY: Yorktown Heights
 STATE: NY
 COUNTRY: USA
 ZIP: 10598-4412
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS 5.0
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/716,942
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/004,157
 FILING DATE: 20-SEP-95
 ATTORNEY/AGENT INFORMATION:
 NAME: Marina T. Larson
 REGISTRATION NUMBER: 32,038
 REFERENCE/DOCKET NUMBER: TERR.P-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 245-1252
 TELEFAX: (914) 962-4330
 TELEX:
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 296
 TYPE: nucleic acid

RESULT 12
 US-09-252-991A-60
 Sequence 60, Application US/09252991A

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; STRANDEDNESS: DOUBLE
; TOPOLOGY: Linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM:
; NAME/KEY: fragment of xylanase gene from degenerate primer
; NAME/KEY: amplification of soil DNA
; US-08-716-942-20

Query Match      52.6%; Score 10; DB 2; Length 296;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy          1 CCAATNNNNNNNNCCACG 19
                  ||||| | | |
Db          217 CCAATGGTGTGGCCACG 199

Search completed: December 4, 2003, 09:58:51
Job time : 79 secs

RESULT 14
US-09-130-337A-20/C
; Sequence 20, Application US/09130337A
; Patent No. 6441148
; GENERAL INFORMATION:
; APPLICANT: Radomska, CCA
; APPLICANT: Seow, KTF
; APPLICANT: Warren, RAJ
; APPLICANT: Yap, WH

; TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
; FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIONS THEREBY
; CURRENT APPLICATION NUMBER: US/09/130,337A
; CURRENT FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 08/116,942
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 60/004,157
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 20
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Description of unknown organism: soil microbe
; US-09-130-337A-20

Query Match      52.6%; Score 10; DB 4; Length 296;
Best Local Similarity 52.6%; Pred. No. 5.5e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy          1 CCAATNNNNNNNNCCACG 19
                  ||||| | | |
Db          217 CCAATGGTGTGGCCACG 199

RESULT 15
US-09-313-294A-7348/C
; Sequence 7348, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PBRL Program

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 09:21:30 ; Search time 254 Seconds

(without alignments)
248.616 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19
Sequence: 1 ccaatnnnnnnccacg 19

Scoring table: IDENTITY NUC

Gpop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0*

Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq;*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUBCOMB.seq;*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUBCOMB.seq;*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	52.6	19 14 US-10-340-759-1	Sequence 1, Appl
c 2	10	52.6	24 11 US-09-940-185-207	Sequence 207, App
c 3	10	52.6	25 9 US-09-402-100-35	Sequence 35, Appl
c 4	10	52.6	25 11 US-09-940-185-4188	Sequence 4188, Ap
c 5	10	52.6	100 10 US-09-969-373-1152	Sequence 1152, AP
6	10	52.6	123 10 US-09-967-701-3962	Sequence 3962, AP
7	10	52.6	136 12 US-09-922-449B-18	Sequence 18, Appl
8	10	52.6	136 12 US-09-322-449B-19	Sequence 19, Appl
9	10	52.6	142 12 US-09-222-449B-8	Sequence 8, Appl
10	10	52.6	143 12 US-09-922-449B-24	Sequence 24, Appl
11	10	52.6	149 12 US-09-322-449B-25	Sequence 25, Appl
12	10	52.6	150 12 US-09-922-449B-10	Sequence 10, Appl
c 13	10	52.6	167 14 US-10-001-883-5	Sequence 5, Appl
c 14	10	52.6	210 10 US-09-374-310-8096	Sequence 8096, Ap
c 15	10	52.6	214 9 US-09-778-320-59	Sequence 59, Appl
c 16	10	52.6	214 9 US-09-910-689-59	Sequence 6226, Ap

ALIGNMENTS

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RESULT 1
US-10-340-759-1
; Sequence 1, Application US-10340759
; Publication No. US20030104575A1
; GENERAL INFORMATION:
;   APPLICANT: HERMONAT, Paul L.
;   APPLICANT: MANE, Michael
;   APPLICANT: LIU, Yong
;   TITLE OF INVENTION: SECRETING PRODUCTS FROM SKIN BY ADENO-ASSOCIATED VIRUS (AAV) GEN
;   TITLE OF INVENTION: TRANSFER
;   FILE REFERENCE: 02533/0116
;   CURRENT APPLICATION NUMBER: US/10/340-759
;   CURRENT FILING DATE: 2003-01-13
;   PRIOR APPLICATION NUMBER: US/09/813, 937A
;   PRIOR FILING DATE: 2001-03-22
;   PRIOR APPLICATION NUMBER: US 60/191092
;   PRIOR FILING DATE: 2000-03-22
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: Patent version 3.1
;   SEQ ID NO: 1
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE: glucose response element
;   OTHER INFORMATION: misc_feature
;   FEATURE: NAME/KEY: misc_feature
;   LOCATION: (6)-(14)
;   OTHER INFORMATION: "N" at positions 6 - 14 can be A, C, G or T
US-10-340-759-1
Query Match Score 52.6%; Score 10; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CGAACNNNNNNNNCCACG 19
Db 1 CGAACNNNNNNNNCCACG 19
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RESULT 2
US-09-940-185-207/c
Sequence 207, Application US/0940185
GENERAL INFORMATION:
; Publication No. US20030096239A1
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 207
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-207

Query Match Score 10; DB 11; Length 24;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
Db 23 CCAATTACGTGACCCAG 5

RESULT 3
US-09-402-100-35/c
Sequence 35, Application US/09402100
GENERAL INFORMATION:
; APPLICANT: Daewoong Pharmaceutical Co, LTD
; APPLICANT: Kim, Byung-O
; APPLICANT: Shin, Sung-Seup
; APPLICANT: Yu, Young-Hyo
; APPLICANT: Park, Myung-Hwan
; APPLICANT: Choi, Deok-Ioon
; APPLICANT: Jung, Hyun-Jin
TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Helio
FILE REFERENCE: 0136/0G140
CURRENT APPLICATION NUMBER: US/09/402,100
; EARLIER APPLICATION NUMBER: KR 97-11950
; EARLIER FILING DATE: 1997-03-31
; EARLIER APPLICATION NUMBER: KR 97-11951
; EARLIER FILING DATE: 1997-03-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: () .() .() .
OTHER INFORMATION: Oligonucleotide

US-09-402-100-35

Query Match Score 10; DB 9; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
Db 23 CCAATTACGTGACCCAG 5

RESULT 4
US-09-940-185-4188/c
Sequence 4188, Application US/0940185
GENERAL INFORMATION:
; Publication No. US20030096239A1
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4188
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4188

Query Match Score 10; DB 11; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
Db 24 CCAATTACGTGACCCAG 6

RESULT 5
US-09-969-373-1152/c
Sequence 1152, Application US/09969373
GENERAL INFORMATION:
; Patent No. US20020133852A1
; APPLICANT: Efferitz, Roger J.
; APPLICANT: Haage, Brian M.
; APPLICANT: Efferitz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10/152679/A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,953
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 1152
LENGTH: 100
TYPE: DNA
ORGANISM: Glycine max
US-09-969-373-1152

Query Match Score 10; DB 11; Length 100;
Best Local Similarity 52.6%; Pred. No. 4.9e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
Db 97 CCAATTACGTGACCCAG 79

RESULT 6
US-09-867-701-3962
Sequence 3962, Application US/09867701

Query Match Score 10; DB 9; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
Db 23 CCAATTACGTGACCCAG 5

Patent No. US20020132237A1
 GENERAL INFORMATION:
 APPLICANT: Aglate, Paul A.
 APPLICANT: Jones, Robert
 APPLICANT: Harlocker, Susan L.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 OF OVARIAN CANCER
 FILE REFERENCE: 210121-497
 CURRENT APPLICATION NUMBER: US/09/867,701
 CURRENT FILING DATE: 2001-05-29
 NUMBER OF SEQ ID NOS: 10912
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3962
 LENGTH: 123
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-867-701-3962

Query Match 52.6%; Score 10; DB 10; Length 123;
 Best Local Similarity 52.6%; Pred. No. 5e+03; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 9;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 4 CCAATCTGTGGGACCAACG 22

RESULT 7
 US-09-922-449B-18

Sequence 18, Application US/0922449B
 Publication No. US20030148278A1.

GENERAL INFORMATION:

APPLICANT: mbH

TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified PCR

FILE REFERENCE: 101215-68

CURRENT APPLICATION NUMBER: US/09/922,449B

PRIOR APPLICATION NUMBER: PCT/EP00/009835

PRIOR FILING DATE: 2000-02-07

PRIOR APPLICATION NUMBER: DE 199 06 169.6

PRIOR FILING DATE: 1999-02-08

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 18

LENGTH: 136

TYPE: DNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the Bt-176

US-09-922-449B-18

OTHER INFORMATION: maize gen

RESULT 8
 US-09-922-449B-19

Sequence 19, Application US/0922449B
 Publication No. US20030148278A1

GENERAL INFORMATION:

APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting

APPLICANT: mbH

TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified PCR

FILE REFERENCE: 101215-68

CURRENT APPLICATION NUMBER: US/09/922,449B

RESULT 8

US-09-922-449B-19
 Sequence 19, Application US/0922449B
 Publication No. US20030148278A1

GENERAL INFORMATION:

APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting

APPLICANT: mbH

TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified PCR

FILE REFERENCE: 101215-68

CURRENT FILING DATE: 2001-08-03

Query Match 52.6%; Score 10; DB 12; Length 142;
 Best Local Similarity 52.6%; Pred. No. 5.1e+03; Indels 9; Gaps 0;
 Matches 10; Conservative 0; Mismatches 9;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 27 CCAATTTCGCTCCACG 45

RESULT 9
 US-09-922-449B-8

Sequence 8, Application US/0922449B
 Publication No. US20030148278A1

GENERAL INFORMATION:

APPLICANT: Bioinside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting

APPLICANT: mbH

TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified PCR

FILE REFERENCE: 101215-68

CURRENT APPLICATION NUMBER: US/09/922,449B

PRIOR APPLICATION NUMBER: PCT/EP00/009835

PRIOR FILING DATE: 2000-02-07

PRIOR APPLICATION NUMBER: DE 199 06 169.6

PRIOR FILING DATE: 1999-02-08

NUMBER OF SEQ ID NOS: 25

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 8

LENGTH: 142

Query Match 52.6%; Score 10; DB 12; Length 142;
 Best Local Similarity 52.6%; Pred. No. 5.1e+03; Indels 9; Gaps 0;
 Matches 10; Conservative 0; Mismatches 9;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 27 CCAATTTCGCTCCACG 45

RESULT 10
 US-09-922-449B-24

Sequence 24, Application US/0922449B
 Publication No. US20030148278A1

GENERAL INFORMATION:

APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting

APPLICANT: mbH

TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified PCR

FILE REFERENCE: 101215-68

CURRENT FILING DATE: 2001-08-03

CURRENT FILING DATE: 2001-08-03

/ PRIOR APPLICATION NUMBER: PCT/EP00/009835
 / PRIOR FILING DATE: 2000-02-07
 / PRIOR APPLICATION NUMBER: DE 199 06 169 . 6
 / PRIOR FILING DATE: 1999-02-08
 / NUMBER OF SEQ ID NOS: 25
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO: 24
 / LENGTH: 143
 / TYPE: DNA
 / ORGANISM: Artificial
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the RRS
 US-09-922-449B-24
 / OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS
 US-09-922-449B-10

	Query Match	Score	DB	Length	Other
Qy	1 CCAATNNNNNNNCCACG 19 1 Db	52.6% Best Local Similarity Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	12 Pred. No. 5.1e+03; Db	143	Score 10; DB 12; Length 143; Pred. No. 5.1e+03; Indels 0; Gaps 0;

RESULT 11
 US-09-922-449B-25
 / Sequence 25, Application US/09922449B
 / Publication No. US20030148278A1
 / GENERAL INFORMATION:
 / APPLICANT: Bioinside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting mbH
 / TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified foodstuff by means of fluorescent-coupled PCR
 / TITLE OF INVENTION: 101215-68
 / FILE REFERENCE: 101215-68
 / CURRENT APPLICATION NUMBER: US/09/922, 449B
 / CURRENT FILING DATE: 2001-08-03
 / PRIOR APPLICATION NUMBER: PCT/EP00/009835
 / PRIOR FILING DATE: 2000-02-07
 / PRIOR APPLICATION NUMBER: DE 199 06 169 . 6
 / PRIOR FILING DATE: 1999-02-08
 / NUMBER OF SEQ ID NOS: 25
 / SEQ ID NO: 25
 / LENGTH: 149
 / TYPE: DNA
 / ORGANISM: Artificial
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS
 US-09-922-449B-25

	Query Match	Score	DB	Length	Other
Qy	1 CCAATNNNNNNNCCACG 19 1 Db	52.6% Best Local Similarity Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	12 Pred. No. 5.1e+03; Db	149	Score 10; DB 12; Length 149; Pred. No. 5.1e+03; Indels 0; Gaps 0;

RESULT 12
 US-09-922-449B-10
 / Sequence 10, Application US/09922449B
 / Publication No. US20030148278A1
 / GENERAL INFORMATION:
 / APPLICANT: Bioinside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting mbH
 / TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified foodstuff by means of fluorescent-coupled PCR
 / FILE REFERENCE: 101215-68
 / CURRENT APPLICATION NUMBER: US/09/922, 449B
 / CURRENT FILING DATE: 2001-08-03
 / PRIOR APPLICATION NUMBER: PCT/EP00/009835
 / PRIOR FILING DATE: 2000-02-07
 / NUMBER OF SEQ ID NOS: 8481

/ PRIOR APPLICATION NUMBER: DE 199 06 169 . 6
 / PRIOR FILING DATE: 1999-02-08
 / NUMBER OF SEQ ID NOS: 25
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO: 10
 / LENGTH: 150
 / TYPE: DNA
 / ORGANISM: Artificial
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS
 US-09-922-449B-10

	Query Match	Score	DB	Length	Other
Qy	1 CCAATNNNNNNNCCACG 19 1 Db	52.6% Best Local Similarity Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	12 Pred. No. 5.1e+03; Db	150	Score 10; DB 12; Length 150; Pred. No. 5.1e+03; Indels 0; Gaps 0;

RESULT 13
 US-10-001-883-5/c
 / Sequence 5, Application US/10001883
 / Publication No. US20030022188A1
 / GENERAL INFORMATION:
 / APPLICANT: Macina, Roberto
 / APPLICANT: Recipon, Herve
 / APPLICANT: Pluta, Jason
 / APPLICANT: Ghosh, Malavika
 / APPLICANT: Sun, Yongming
 / APPLICANT: Liu, Chenghua
 / TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro
 / FILE REFERENCE: DEX-0271
 / CURRENT APPLICATION NUMBER: US/10/001, 883
 / CURRENT FILING DATE: 2001-11-20
 / PRIOR APPLICATION NUMBER: 60/252, 059
 / PRIOR FILING DATE: 2000-11-20
 / NUMBER OF SEQ ID NOS: 137
 / SEQ ID NO: 5
 / LENGTH: 167
 / TYPE: DNA
 / ORGANISM: Homo sapien
 US-10-001-883-5

	Query Match	Score	DB	Length	Other
Qy	1 CCAATNNNNNNNCCACG 19 1 Db	52.6% Best Local Similarity Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	12 Pred. No. 5.2e+03; Db	167	Score 10; DB 14; Length 167; Pred. No. 5.2e+03; Indels 0; Gaps 0;

RESULT 14
 US-09-974-300-8096/c
 / Sequence 8096, Application US/09974300
 / Patent No. US20030146721A1
 / GENERAL INFORMATION:
 / APPLICANT: Berka, Randy M.
 / APPLICANT: Clausen, Ib Groth
 / TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 / FILE REFERENCE: 10085-500-US
 / CURRENT APPLICATION NUMBER: US/09/974, 300
 / CURRENT FILING DATE: 2001-10-05
 / PRIOR APPLICATION NUMBER: 60/680, 598
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 60/279, 526
 / PRIOR FILING DATE: 2001-03-27
 / NUMBER OF SEQ ID NOS: 8481

/ PRIOR APPLICATION NUMBER: DE 199 06 169 . 6
 / PRIOR FILING DATE: 1999-02-08
 / NUMBER OF SEQ ID NOS: 25
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO: 10
 / LENGTH: 150
 / TYPE: DNA
 / ORGANISM: Artificial
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS
 US-09-974-300-8096/c

	Query Match	Score	DB	Length	Other
Qy	1 CCAATNNNNNNNCCACG 19 1 Db	52.6% Best Local Similarity Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	12 Pred. No. 5.2e+03; Db	150	Score 10; DB 12; Length 150; Pred. No. 5.2e+03; Indels 0; Gaps 0;

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 8096 LENGTH: 210
 TYPE: DNA
 ORGANISM: Bacillus clausii
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1) ..(210)
 OTHER INFORMATION: n = A,T,C or G
 US-09-974-300-8096

Query Match Score 10; DB 10; Length 210;
 Best Local Similarity 52.6%; Pred. No. 5.3e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 152 CCAATTCTGTCTGCACG 134

RESULT 15
 US-09-778-320-59/c
 Sequence 59, Application US/09778320
 Patent No. US2010034052A1
 GENERAL INFORMATION:
 APPLICANT: Dillon, Davin C.
 APPLICANT: Day, Craig H.
 APPLICANT: Jiang, Yugiu
 APPLICANT: Houghton, Raymond L.
 APPLICANT: Mitcham, Jennifer
 APPLICANT: Wang, Tongrong
 APPLICANT: MCNEILL, Patricia D.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
 FILE REFERENCE: 210121.491C5
 CURRENT APPLICATION NUMBER: US/09/778,320
 CURRENT FILING DATE: 2001-02-06
 NUMBER OF SEQ ID NOS: 301
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 59
 LENGTH: 214
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1) ..(214)
 OTHER INFORMATION: n = A,T,C or G
 US-09-778-320-59

Query Match Score 10; DB 9; Length 214;
 Best Local Similarity 52.6%; Pred. No. 5.3e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 88 CCAATTCTCATTCACCG 70

Search completed: December 4, 2003, 10:57:37
 Job time : 257 secs

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 05:58:56 ; Search time 2068 Seconds
(without alignments)

BQ23.300 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19

Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

```

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_esro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_name:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rid:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssi:*
29: gb_gss1:*

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RESULT 1

BH857113 LOCUS SALK_076821.44.95.x

DEFINITION Arabidopsis thaliana genomic clone SALK_076821.44.95.x, genomic survey sequence.

ACCESSION BH857113

VERSION GSS.

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 43)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished

COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

ALIGNMENTS

BQ756881 EBem09_sq
AL897168 AL897168
BH251489 SALK_0116
BQ09298 ph28h02.y
BH232183 100616.D1
BH22106 100110.S1
CB338675 kb5b04.y
A2921866 HRCot4D10
BF086094 CM3_GN005
BF086094 CM3_GN005
AA927925 on23b01.s
BH864991 SALK_0972
BF094257 CM4_UT004
A2720239 RPCI-24-1
BZ662888 SALK_0263
BH22899 100610.RH
CC458196 SALK_1171
A1938545 sb55b02.y
AW945325 PM3_EN000
BG950375 CM3-CT006
BW091136 BW091136
CC029017 3591_1-10
AG024826 Oryza sat
CC037007 3591_1-84
A1549504 UI-R-C3-T
BH230343 1006157D1
BH905244 SALK_1057
CC097190 AF53_Rpf
BH222096 100610.C0
AA405167 2551h01..r
AQ073902 EP (3).1309
BH812753 SALK_0630
BH847929 SALK_0660
A2913927 1006017C0
BH895687 3526_1_35
BZ663067 SALK_0765
B2386507 EINAF75TR
BF361951 QV2-NN004
BE936064 QV2-NN005
BH751521 SALK_0292
BH854781 SALK_0886

RESULTS

1

BH857113 LOCUS SALK_076821.44.95.x

DEFINITION Arabidopsis thaliana TDNA insertion lines

survey sequence.

BH857113

GSS.

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 43)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J., and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished

COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Result No.	Score	Query Match length	DB ID	Description
1	10	52.6	43 28 BH857113	BH857113 SALK_0768
C 2	10	52.6	47 29 BX92617	BX92617 Arabidops
C 3	10	52.6	58 22 AL949322	AL949322 Arabidops
C 4	10	52.6	76 9 AA475936	AA475936 vh25b10.r

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARES

4

Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g29100.
 Class: TDNA tagged.

FEATURES	Source
	1..43
	/organism="Arabidopsis thaliana" /mol type="genomic DNA" /strain="columbia 0" /db_xref="taxon:3702" /clone="SALK_076821_44_95.x" /clone_id="Arabidopsis thaliana TDNA insertion lines" /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html "
BASE COUNT	11 a 11 c 10 g 11 t
ORIGIN	

Query Match Score 10; DB 28; Length 43;
 Best Local Similarity Pred No. 1e+04;
 Max Local Similarity Max No. 1e+04;

JOURNAL REFERENCE	Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K., and Weisshaar, B.
AUTHORS	A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
TITLE	for flanking sequence tag based reverse genetics
JOURNAL	Unpublished
AUTHORS	Unpublished
TITLE	Unpublished
JOURNAL	Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
AUTHORS	This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F1913. The sequences are generated at the MDT for Plant Breeding and Biotechnology, Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
TITLE	
JOURNAL	
COMMENT	

Plant Genomics program designated 'GABI'. Availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

flanking the insertion. Sequences displaying significant similarity to the *A. thaliana* nuclear genome sequence were processed for submission. T-DNA derived sequences were

	BASE COUNT	21	a	11	c	10	g	16	t
	ORIGIN	Removed							
Query	Match	52.6%		Score 10;	DB 29;	Length 58;			
	Best Local Similarity	52.6%		Pred. No. 2:3e+04;					
	Matches	10;	Conservative	0; Mismatches	9;	Indels 0;	Gaps 0;		
Qy		1	CCAAATNNNNNNNNNNCCACG 19						
Db		34	CCAAATTGTGGTAGCCACG 16						

RESULT 4
 AA475936
 LOCUS
 vh25b10_r1
 DEFINITION
 Soares mammary gland NbMG Mus musculus cDNA clone
 IMAGE:176475 5, similar to TR:E196749 E196749 mRNA; EXPRESSED
 SEQUENCE TAG ; mRNA sequence.
 AA475936
 AA475936.1
 EST
 GI:2203787
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurgnathi; Muridae; Murinae; Mus.
 KEYWORD
 1 (bases 1 to 16)
 Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le M., Martin, J., Morris, M.,
 Scheinfeld, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wyly, T., Lennon, G., Soares, B., Wilson, R., and
 Waterston, R.
 THE WASHU HUMT Mouse EST Project
 TITLE

JOURNAL Unpublished
COMMENT Contact : Marra M/Mouse EST Project
WashU HMMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:15955
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq. primer: -28m13 rev2 ET from Amersham
High Quality sequence available at:
<http://www.ncbi.nlm.nih.gov/blast/>

BASE COUNT	19	a	28	c	16	9	13	t
ORIGIN								
Query Match	52.6%		Score 10;	DB 9;	Length 76;			
Best Local Similarity	52.6%		Pred. No. 2.6e+04;					
Matches	10;	Conservative	0;	Mismatches 9;	Indels			
Qy	1	CCATNNNNNNNNNNCCACG	19					
Db	40	CCAATGGTTAGGCCACG	58					
RESULT 5								
LOCUS	BQ756881	BQ756881	79 bp	mRNA	linear			
DEFINITION	EBem09_SQ005_E15_R	embryo, 1 Day Germination, no tr						
Organism	Eukaryota; Viridiplantae; Streptophyta; Embryophyta							
Keywords	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Po							
REFERENCE	1	(bases 1 to 79)						
AUTHORS	Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, R., Ramsay, L., Machray G., Marshall, D.F.M. and Waugh, R.							
TITLE	Unpublished							
JOURNAL	Development of Barley Transcriptome Resources							
COMMENT	Contact: Waugh R, Marshall DF							
	Genome Dynamics/Computational Biology							
	Scottish Crop Research Institute							
	Invergowrie, Dundee, DD2 5DA, Scotland, UK							
	Tel: 00 44 1382 562731							
	Fax: 00 44 1382 562426							
	Email: est@scri.sari.ac.uk.							
FEATURES	source	Location/Qualifiers	1..79					
	/organism="Hordeum vulgare subsp. vulgare"							
	/mol_type="mRNA"							
	/cultivar="Optic"							
	/db_xref="taxon:112509"							
	/clone="EBem09_SQ005_E15"							
	/tissue_type="embryo"							
	/dev_stage="1 Day germination"							
	/lab_host="DH10B"							
	/clone.lib="embryo, 1 Day germination, no tr							
	Optic, EBem09"							
	/note="Vector: PSORT1; Site_1: Sal I; Site_2: Sma I; Non-normalised library; directionally cloned"							
	Derived from embryos dissected from germinating barley in glasshouse grown barley plants. Development of the barley transcriptome resources of Barley funded cereal IGF (Investigating Gene Function)							
BASE COUNT	19	a	18	c	17	9	25	t
ORIGIN								
Query Match	52.6%		Score 10;	DB 13;	Length 79;			
Best Local Similarity	52.6%		Pred. No. 2.6e+04;					
Matches	10;	Conservative	0;	Mismatches 9;	Indels			
Qy	1	CCATNNNNNNNNNNCCACG	19					
Db	42	CCAATTGGCAACACG	60					
RESULT 6								
LOCUS	AL897168/c	AL897168	80 bp	mRNA	linear			

revealed the presence of an additional Trichostrongyloidea cestode nematode, *Cooperia oncophora*. Sequences in this library may derive from either Ostertagia or Cooperia.*** The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR library was made using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMP1. Nematodes were provided by Dr. Louis Gasparre of the USDA, Beltsville, MD (lgasbar@anri.barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of Ostertagia eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen.**

24 a 24 c 12 g 22 t

BASE COUNT ORIGIN

Query Match BH232183/C

Best Local Similarity 52.6%; Score 10; Length 82;

Matches 10; Conservative Pred. No. 2.6e+04;

0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19

Db 12 CCAATGGAGTGTCCACG 30

RESULT 9 BH232183/C

LOCUS BH232183 Y1 1006 - RescueMu Grid G Zea mays genomic, genomic

DEFINITION survey sequence.

ACCESSION BH232183

VERSION BH232183.1

KEYWORDS GI:16837119

SOURCE GSS,

ORGANISM Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 97)

AUTHORS Walbot, V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished

COMMENT Contact: Walbot, V.

Unpublished

CONTACT Walbot, V.

Department of Biological Sciences

Stanford University

Ave, Palo Alto, CA 94304, USA

Phone: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1006105 row: 13

Class: transposon-tagged

Location/Qualifiers

1. .97

FEATURES source

Organism="Zea mays"

/mol type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="106 - RescueMu Grid G"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin.**

BASE COUNT 13 a 24 c 37 g 12 t

ORIGIN

Query Match BH222106/C

Best Local Similarity 52.6%; Score 10; Length 86;

Matches 10; Conservative Pred. No. 2.6e+04;

0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19

Db 61 CCAATCATGGACGCCACG 43

RESULT 10 BH222106/C

LOCUS BH222106

DEFINITION 1006105C10.x1 1006 - RescueMu Grid G Zea mays genomic, genomic

DEFINITION SURVEY sequence.

ACCESSION BH222106

VERSION BH222106.1

KEYWORDS GI:16816606

SOURCE GSS,

ORGANISM Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 86)

AUTHORS Walbot, V.

Title Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished

COMMENT Contact: Walbot, V.

Department of Biological Sciences

Stanford University

Ave, Palo Alto, CA 94304, USA

Phone: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.

Plate: 1006166 row: 23

Class: transposon-tagged

Location/Qualifiers

1. 86

FEATURES source

Organism="Zea mays"

/mol type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="106 - RescueMu Grid G"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

BASE COUNT 11 a 27 c 44 g 15 t

ORIGIN

Query Match 52.6%; Score 10; DB 28;

Pred. No. 2.8e+04; Length 97;

REFERENCE AUTHORS
Euukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates;
1 (bases 1 to 100) Dias Neto,E., Garcia Correa,R., Verjovskii-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,P.F.,
Brunstein,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 2002663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?i=&t=2-CM3-GN0052-080
900-334-c11&t3=2000-09-08&t4=1)
Seq. primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 100.
Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0052"
/note="Organ: placenta-normal; Vector: puc18; Site_1: Small
Site_2: Small; A mini-library was made by cloning_1: Small
products derived from QRESNES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the PUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT ORIGIN
35 a 23 c 18 g . 24 t

FEATURES source
Query Match Score 10; DB 10; Length 100;
Best Local Similarity 52.6%; Pred. No. 2.8e+04;
Matches 10; Conservative 0; Mismatches . 9; Indels 0; Gaps 0;
/DEFINITION BOGXN16T BOGX Brassica oleracea genomic clone BOGXN16, genomic
SURVEY SEQUENCE
ACCESSION BH583741
VERSION BH583741.1
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Euukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 101)
REFERENCE Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
AUTHORS Unpublished shotgun sequencing of *Brassica oleracea*
TITLE Contact: Chris Town
JOURNAL COMMENT

REFERENCE AUTHORS
Euukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates;
1 (bases 1 to 100) Dias Neto,E., Garcia Correa,R., Verjovskii-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,P.F.,
Brunstein,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 2002663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?i=&t=2-CM3-GN0052-080
900-334-c11&t3=2000-09-08&t4=1)
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High quality sequence start: 5
High quality sequence stop: 100.
Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0052"
/note="Organ: placenta-normal; Vector: puc18; Site_1: Small
Site_2: Small; A mini-library was made by cloning_1: Small
products derived from QRESNES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the PUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT ORIGIN
35 a 23 c 18 g . 24 t

FEATURES source
Query Match Score 10; DB 10; Length 100;
Best Local Similarity 52.6%; Pred. No. 2.8e+04;
Matches 10; Conservative 0; Mismatches . 9; Indels 0; Gaps 0;
/DEFINITION BOGXN16T BOGX Brassica oleracea genomic clone BOGXN16, genomic
SURVEY SEQUENCE
ACCESSION BH583741
VERSION BH583741.1
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Euukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 101)
REFERENCE Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
AUTHORS Unpublished shotgun sequencing of *Brassica oleracea*
TITLE Contact: Chris Town
JOURNAL COMMENT

REFERENCE AUTHORS
Euukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates;
1 (bases 1 to 100) Dias Neto,E., Garcia Correa,R., Verjovskii-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,P.F.,
Brunstein,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and
Simpson,A.J.

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MEDLINE 2002663
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COMMENT Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

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(http://www.ludwig.org.br/scripts/gethtml2.pl?i=&t=2-CM3-GN0052-080
900-334-c11&t3=2000-09-08&t4=1)
Seq. primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 100.
Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0052"
/note="Organ: placenta-normal; Vector: puc18; Site_1: Small
Site_2: Small; A mini-library was made by cloning_1: Small
products derived from QRESNES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the PUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT ORIGIN
35 a 23 c 18 g . 24 t

FEATURES source
Query Match Score 10; DB 10; Length 100;
Best Local Similarity 52.6%; Pred. No. 2.8e+04;
Matches 10; Conservative 0; Mismatches . 9; Indels 0; Gaps 0;
/DEFINITION BOGXN16T BOGX Brassica oleracea genomic clone BOGXN16, genomic
SURVEY SEQUENCE
ACCESSION BH583741
VERSION BH583741.1
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Euukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 101)
REFERENCE Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
AUTHORS Unpublished shotgun sequencing of *Brassica oleracea*
TITLE Contact: Chris Town
JOURNAL COMMENT

REFERENCE AUTHORS
Euukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates;
1 (bases 1 to 100) Dias Neto,E., Garcia Correa,R., Verjovskii-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,P.F.,
Brunstein,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 2002663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?i=&t=2-CM3-GN0052-080
900-334-c11&t3=2000-09-08&t4=1)
Seq. primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 100.
Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0052"
/note="Organ: placenta-normal; Vector: puc18; Site_1: Small
Site_2: Small; A mini-library was made by cloning_1: Small
products derived from QRESNES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the PUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT ORIGIN
35 a 23 c 18 g . 24 t

FEATURES source
Query Match Score 10; DB 10; Length 100;
Best Local Similarity 52.6%; Pred. No. 2.8e+04;
Matches 10; Conservative 0; Mismatches . 9; Indels 0; Gaps 0;
/DEFINITION BOGXN16T BOGX Brassica oleracea genomic clone BOGXN16, genomic
SURVEY SEQUENCE
ACCESSION BH583741
VERSION BH583741.1
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Euukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 101)
REFERENCE Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
AUTHORS Unpublished shotgun sequencing of *Brassica oleracea*
TITLE Contact: Chris Town
JOURNAL COMMENT

```

BASE COUNT      25 Soares and M. Fatima Bonaldo.
ORIGIN          a 23 c 25 g 30 t
Query Match    52.6%; Score 10; DB 9;
Best Local Similarity 52.6%; Pred. No. 2.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Caps 0;
Qy   1 CCAATNNNNNNNNCCACG 19
||||||| |

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Search completed: December 4, 2003, 07:47:50
Job time : 2077 secs

Result No.	Query Match Score	Length	DB ID	Description
1	10	52.6	BH857113	BH857113 SALK_0768
2	10	52.6	47	29 BX29617 Arabidopsis
3	10	52.6	58	29 AL949322 Arabidopsis
4	10	52.6	76	9 AA47936 Arabidopsis

Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g29100.

Class: TDNA tagged.

FEATURES

Source	Location/Qualifiers
1 -43	/organism="Arabidopsis thaliana" /mol_type="genomic DNA" /strain="Columbia 0" /db_xref="taxon:3702" /clone lib="Arabidopsis thaliana TDNA insertion lines" /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tDNA_protocols.html "

BASE COUNT

ORIGIN	11 a	11 C	10 g	11 t
Query Match	52.6%	Score 10;	DB 28;	Length 43;
Best Local Similarity	52.6%	Pred. No 2e+04;	0;	Gaps 0;
Matches	10;	Conservative	0;	
Db	18	CCATGAAATTACCCACG	19	36

RESULT 3

AL949322/C	LOCUS	58 bp	DNA linear	GSS 24-OCT-2002
AL949322	Arabidopsis thaliana T-DNA Flanking sequence GK-319H03-015860,			
	Genomic Survey Sequence.			
	AL949322	GI: 24405944		
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM	Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicaeae; Arabidopsis.				
Strizhov, N., Li, Y., Rosso, M., Viehöver, P., Dekker, K., Saedler, H. and Weisshaar, B.				
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines				
Unpublished				
REFERENCE				
AUTHORS	Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K., and Weisshaar, B.			
TITLE	A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat).			
JOURNAL	Submitted (21-OCT-2002) Weisshaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany			
COMMENT	This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At1g50730. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ .			

FEATURES

Source	
1 -47	/organism="Arabidopsis thaliana" /mol type="genomic DNA" /strain="Columbia 0" /db_xref="taxon:3702"

FEATURES

Source	
1	/organism="Arabidopsis thaliana" /mol type="genomic DNA" /strain="Columbia 0" /db_xref="taxon:3702"

/clone="GK-455E08-018778"
/cclone lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment (8) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT

ORIGIN	17 a	4 c	10 g	16 t
Query Match	52.6%	Score 10;	DB 29;	Length 47;
Best Local Similarity	52.6%	Pred. No. 2.1e+04;	0;	
Matches	10;	Conservative	0;	
Qy	1	CCATNNNNNNNNCCACG	19	
Db	22	CCGATAAAAACCTCTCACG	4	

RESULT 3

AL949322/C	LOCUS	58 bp	DNA linear	GSS 24-OCT-2002
AL949322	Arabidopsis thaliana T-DNA Flanking sequence GK-319H03-015860,			
	Genomic Survey Sequence.			
ACCESSION	AL949322	GI: 24405944		
VERSION				
KEYWORDS				
SOURCE				
ORGANISM	Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicaeae; Arabidopsis.				
Strizhov, N., Li, Y., Rosso, M., Viehöver, P., Dekker, K., Saedler, H. and Weisshaar, B.				
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines				
Unpublished				
REFERENCE				
AUTHORS	Rosso, M., Strizhov, N., Li, Y., and Weisshaar, B.			
TITLE	A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat).			
JOURNAL	Submitted (21-OCT-2002) Weisshaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany			
COMMENT	This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F1913. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ .			

FEATURES

Source	
1	/organism="Arabidopsis thaliana" /mol type="genomic DNA" /strain="Columbia 0" /db_xref="taxon:3702"

FEATURES

Source	
1	/organism="Arabidopsis thaliana" /mol type="genomic DNA" /strain="Columbia 0" /db_xref="taxon:3702"

flanking the insertion. Sequences displaying significant similarity to the *A. thaliana* nuclear genome sequence were processed for submission. T-DNA derived sequences were

	BASE COUNT	21	a	11	c	10	g	16	t	
	ORIGIN									
y	Query Match	52.6%		Score 10;	DB 29;	Length 58;				
	Best Local Similarity	52.6%		Prc. No.	2.3e+04;					
	Matches 10;	Conservative		0;	Mismatches 9;	Indels 0;	Gaps 0;			
b	1	CCAAATNNNNNNNNCCACG	19							
	34	CCAAATCTGTGTAGCCACG	16							

RESULT	4
A45936	
OCUS	AA475936
DEFINITION	76 bp mRNA vh2b10_r1 Soares mammary gland NbDMG MuS muscle CDNA clone IMAGE: B71475 5' similar to TR_E196749 E196749 MRNA; EXPRESSED SEQUENCE TAG ; mRNA sequence.
ACCESSION	AA475936
VERSION	AA475936.1
KEYWORDS	EST
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
EULER	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eurelomontomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Murinae; Mus.
REFERENCE	1 (bases 1 to 76)
AUTHORS	Marra, M., Hillier, L.L., Bowles, M., Dietrich, N., Morris, J.M., Martin, J., Le, M., Lacy, M., Steptoe, M., Tan, F., Underwood, K., Moore, B., Scheibenbogen, K.

Waterson, R.,
The WashU-HHMI Mouse EST Project
Unpublished
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 85001, St. Louis, MO 63108
TITLE
JOURNAL
COMMENT

tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This Clone is available royalty-free through LLNL ; contact the
IMAG Consortium (info@image.llnl.gov) for further information.
MGI: 511955
Trace considered Overall near binary.

Possible reverted clone: similarity on wrong strand
 Seq. Primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..76

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/mol type="mRNA"
/strain="C57BL/6J"
/db_xref="Taxon:10090"
/clone="IMAGE:876475"
/sex="male"
/tissue_label="mammary gland"
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BASE COUNT ORIGIN 19 a 28 C 16 g 13 t
ORIGIN 19 a 28 C 16 g 13 t

RESULT 5
 BQ756881 LOCUS BQ756881 linear EST 26-JUL-2001
 DEFINITION EBemo9_S0005_E15_R embryo, 1 Day germination, no treatment, cv Optic, _EBemo9_Hordium vulgare subsp. vulgare cDNA clone

REFERENCE : (bases 1 to 79)
 AUTHORS : Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
 Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
 TITLE : Development of Barley Transcriptome Resources
 JOURNAL : Unpublished
 COMMENT : Contact: Waugh R, Marshall DF, Cardle L, Liu H, Caldwell D, McCallum N, Mudie S, Ramsay L, Machray G, Marshall DFM, and Hedley P

```

/organism="Hordeum vulgare subsp. vulgaris"
/mol type="mRNA"
/cultivar="Optic"
/db xref="JAXON:112509"
/clone="EPEM09_SQ005_E15"
/tissue_type="embryo"
/dev_stage="1 day germination"
/lab_boss="Inaki"

```

/clone_1.lib="embryo", 1 Day germination, no treatment, cv Optic, BBSR09"
 /notes="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
 Non-normalised library, directionally cloned into pSPORT1.
 Derived from embryos dissected from germinating grains (1 day) in Glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal 17G (Investigating Gene Function) project."
 19 a 18 C 17 g 25 t
 BASE COUNT

ORIGIN	Qy	Db	Query Match	52.6%	Score 10;	DB 13;	Length 79;
			Best Local Similarity	52.6%	Pred. No.	2.6e+04;	
			Matches 10;	Conservative	0;	Mismatches 9;	Indels 0;
							Gaps 0;
	1	41	CCAAATNNNNNNNNCCACG	19			
	42	42	CCAAATTGTCAAACACG	60			

RESULT 6 AL897168/c LOCUS AL897168 DDPMV..... 80 bp mRNA linear EST 16-SEP-2002

revealed the presence of an additional Trichostrongyloidea cattie nematode, *Cooperia oncophora*. Sequences in this library may derive from either *Ostertagia* or *Cooperia*.*** The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pMPL. Nematodes were provided by Dr. Louis Gasbarre of the USDA, Beltsville, MD (lgasbarre@nri.barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of *Ostertagia* eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen.**

24 a 24 c 12 g 22 t

BASE COUNT ORIGIN

Query Match BH232183/C

LOCUS BH232183

DEFINITION 1006166D12.Y1.1006 - Rescuemu Grid G Zea mays genomic, genomic survey sequence.

ACCESSION BH232183

VERSION BH232183.1

KEYWORDS GI:168337119

SOURCE GSS.

ORGANISM Zea mays

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

SPERMATOPHYTA; Magnoliophyta; Liliopsida; Poaceae; PACCAD

CLADE; Panicoideae; Andropogoneae; Zea.

FEATURES 1. (bases 1 to 86)

REFERENCE Walbot, V.

AUTHORS Unpublished

JOURNAL Contact: Walbot, V.

COMMENT Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Phone: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1006105 row: 13

Class: transposon-tagged

Location/Qualifiers 1. .97

FEATURES Source

REFERENCE 1. "Zea mays"

AUTHORS /mol type="genomic DNA"

JOURNAL /cultivar="mixed background W23/A188/B73"

COMMENT /tissue type="leaf"

/dev stage="adult"

/lab host="DH10B"

Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.

Plate: 1006166 row: 23

Class: transposon-tagged

Location/Qualifiers 1. .86

FEATURES Source

REFERENCE 1. "Zea mays"

AUTHORS /mol type="genomic DNA"

JOURNAL /cultivar="mixed background W23/A188/B73"

COMMENT /tissue type="leaf"

/dev stage="adult"

/lab host="DH10B"

/clone lib=1006 - Rescuemu Grid G"

note=Organ: leaf; Vector: Rescuemu (engineered from

PBlueScript backbone); Site 1: BamHI; Site 2: BglII;

Rescuemu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT ORIGIN

Query Match BH222106/C

LOCUS BH222106

DEFINITION 1006105C10.X1.1006 - Rescuemu Grid G Zea mays genomic, genomic survey sequence.

ACCESSION BH222106

VERSION BH222106.1

KEYWORDS GI:16816606

SOURCE GSS

ORGANISM Zea mays

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

SPERMATOPHYTA; Magnoliophyta; Liliopsida; Poaceae; PACCAD

CLADE; Panicoideae; Andropogoneae; Zea.

FEATURES 1. (bases 1 to 97)

REFERENCE Walbot, V.

AUTHORS Unpublished

JOURNAL Contact: Walbot, V.

COMMENT Department of Biological Sciences

Stanford University

85 California Ave, Palo Alto, CA 94304, USA

Phone: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1006105 row: 13

Class: transposon-tagged

Location/Qualifiers 1. .97

FEATURES Source

REFERENCE 1. "Zea mays"

AUTHORS /mol type="genomic DNA"

JOURNAL /cultivar="mixed background W23/A188/B73"

COMMENT /tissue type="leaf"

/dev stage="adult"

/lab host="DH10B"

Rescuemu (engineered from PBlueScript backbone), Site 1: BamHI, Site 2: BglII, designed to allow plasmid rescue from total genomic DNA.

BASE COUNT ORIGIN

Query Match BH222106/C

LOCUS BH222106

DEFINITION 1006105C10.X1.1006 - Rescuemu Grid G Zea mays genomic, genomic survey sequence.

ACCESSION BH222106

VERSION BH222106.1

KEYWORDS GI:16816606

SOURCE GSS

ORGANISM Zea mays

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

SPERMATOPHYTA; Magnoliophyta; Liliopsida; Poaceae; PACCAD

CLADE; Panicoideae; Andropogoneae; Zea.

FEATURES 1. (bases 1 to 97)

REFERENCE Walbot, V.

AUTHORS Unpublished

JOURNAL Contact: Walbot, V.

COMMENT Department of Biological Sciences

Stanford University

85 California Ave, Palo Alto, CA 94304, USA

Phone: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1006105 row: 13

Class: transposon-tagged

Location/Qualifiers 1. .97

FEATURES Source

REFERENCE 1. "Zea mays"

AUTHORS /mol type="genomic DNA"

JOURNAL /cultivar="mixed background W23/A188/B73"

COMMENT /tissue type="leaf"

/dev stage="adult"

/lab host="DH10B"

Rescuemu (engineered from PBlueScript backbone), Site 1: BamHI, Site 2: BglII, designed to allow plasmid rescue from total genomic DNA.

Matches	10;	Conservative	0;	Mismatches	9;	Indels	0;	Gaps	0;	DEFINITION	HRCot4D10 Sorghum bicolor HRCot Sorghum bicolor genomic, genomic survey sequence.
Qy	1 CCAATNNNNNNNNCCACG 19									ACCESSION	A2921866
Db	92 CCAATTGGAGCACCCACCG 74									VERSION	GI:13400225
										KEYWORDS	GSS
										SOURCE	Sorghum bicolor (sorghum)
										ORGANISM	Sorghum bicolor
RESULT 11										Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.	
LOCUS	CB338675	99 bp	mRNA	linear	EST 13-MAR-2003					REFERENCE	1 (bases 1 to 99)
DEFINITION	rb59b04.y1 Brugia malayi L3 pAMP1 v2 Brugia malayi CDNA 5' similar to TR_O16159 O16159 CYSTATIN-TYPE CYSTEINE PROTEINASE INHIBITOR. ;, mRNA sequence.									AUTHORS	Peterson,D.G., Schulze,S.R., Sciara,E.B., Lee,S.A., Bowers,J.E., Nagel,A., Jiang,N., Tibbitts,D.C., Wessler,S.R. and Paterson,A.H.
ACCESSION	CB338675									TITLE	Integration of Cot analysis, DNA cloning, and high-throughput sequencing facilitates genome characterization and gene discovery
VERSION	CB338675.1									JOURNAL	Genome Res. 12 (5), 795-807 (2002)
KEYWORDS	EST.									MEDLINE	21992826
SOURCE	Brugia malayi									PUBMED	11997346
ORGANISM	Brugia malayi									COMMENT	Contact: Peterson DG Plant Genome Mapping Laboratory University of Georgia Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA 30602, USA Tel: 706-583-0167 Fax: 706-583-0160 Email: dpg@arches.uga.edu
										CLASS	Hydroxylapatite-fractionated DNA
										FEATURES	Location/Qualifiers
										1.	.99
										source	/organism="Sorghum bicolor" /mol_type="genomic DNA" /clustVector="BTXc23" /db_xref="Laxxon.4558" /dev_stage="seeds" /tissue_type="leaves" /clone_id="Sorghum bicolor HRCot" /note="vector: pGEM-TA-Easy; A Cot analysis was performed for the sorghum genome. Based on the resulting Cot curve, hydroxyapatite chromatography was used to isolate moderately-repetitive (MR), and single/low copy, (SL) sequence components from sheared genomic DNA. The three repetition-based DNA HRCot, and SLcot genomic libraries. Blotting and sequencing data indicates that each library is representative of the component from which it was derived. Putative ID listings given for sequences are based on comparison (blastn) with sequences in the NCBI NR database. Only the primary match is given (all primary E values are < or = 1.00E-5). In no instance does a 'Cot clone' contain the complete sequence of its putative Nr match."
										BASE COUNT	18 a 19 c 29 g 33 t
										ORIGIN	Query Match Score 10; DB 28; Length 99; Best Local Similarity 52.6%; Pred. No. 2.8e+04; Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
										Qy	1 CCAATNNNNNNNNCCACG 19
										Db	56 CCAATGCAATCTCCACG 38
										RESULT 13	
										LOCUS	BF086094
										DEFINITION	CM3-GN0052-080900-334-c11
										ACCESSION	BF086094
										VERSION	BF086094
										KEYWORDS	EST.
										SOURCE	Homo sapiens (human)
										ORGANISM	Homo sapiens

REFERENCE AUTHORS
Euukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
Dias Neto, E., Garcia Correa, R., Verjovskii-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W.J.R., Zago, M.A., Bordim, S., Costa, F.F.,
Goldstein, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t=CM3-GN0052-0809&0-334/c11ct3=200-09-08&c4=1>)

Seq primer: puc 18 forward

High quality sequence start: 5

High quality sequence stop: 100.

Location/Qualifiers

1 .100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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/note="Organ: Placenta; normal; Vector: puc18; Site_1: Small site 2: Smal; A mini library was made by cloning productS derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) Profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES source

LOCUS BH583741

DEFINITION BOGAN6TR BOGX Brassica oleracea genomic clone BOCXN16, genomic survey sequence.

ACCESSION BH583741

VERSION GI:17836198

KEYWORDS GSS

ORGANISM Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 101)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

AUTHORS

TITLE Whole genome shotgun sequencing of *Brassica oleracea*

JOURNAL Unpublished

COMMENT Contact: Chris Town

RESULT 14

LOCUS BH583741

DEFINITION BOGAN6TR BOGX Brassica oleracea genomic clone BOCXN16, genomic survey sequence.

ACCESSION BH583741

VERSION GI:17836198

KEYWORDS GSS

ORGANISM Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Brassica.

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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

AUTHORS

TITLE Whole genome shotgun sequencing of *Brassica oleracea*

JOURNAL Unpublished

COMMENT Contact: Chris Town

REFERENCE AUTHORS
Euukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
Dias Neto, E., Garcia Correa, R., Verjovskii-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W.J.R., Zago, M.A., Bordim, S., Costa, F.F.,
Goldstein, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t=CM3-GN0052-0809&0-334/c11ct3=200-09-08&c4=1>)

Seq primer: puc 18 forward

High quality sequence start: 5

High quality sequence stop: 100.

Location/Qualifiers

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/mol_type="mRNA"
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/dev_stage="Adult"
/clone_lib="GN0052"
/note="Organ: Placenta; normal; Vector: puc18; Site_1: Small site 2: Smal; A mini library was made by cloning productS derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) Profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES source

LOCUS BH583741

DEFINITION BOGAN6TR BOGX Brassica oleracea genomic clone BOCXN16, genomic survey sequence.

ACCESSION BH583741

VERSION GI:17836198

KEYWORDS GSS

ORGANISM Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 101)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

AUTHORS

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JOURNAL Unpublished

COMMENT Contact: Chris Town

RESULT 14

LOCUS BH583741

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ACCESSION BH583741

VERSION GI:17836198

KEYWORDS GSS

ORGANISM Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 101)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

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JOURNAL Unpublished

COMMENT Contact: Chris Town

REFERENCE AUTHORS
Euukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
Dias Neto, E., Garcia Correa, R., Verjovskii-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W.J.R., Zago, M.A., Bordim, S., Costa, F.F.,
Goldstein, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t=CM3-GN0052-0809&0-334/c11ct3=200-09-08&c4=1>)

Seq primer: puc 18 forward

High quality sequence start: 5

High quality sequence stop: 100.

Location/Qualifiers

1 .100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0052"
/note="Organ: Placenta; normal; Vector: puc18; Site_1: Small site 2: Smal; A mini library was made by cloning productS derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) Profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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VERSION GI:17836198

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Brassica.

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JOURNAL Unpublished

COMMENT Contact: Chris Town

RESULT 14

LOCUS BH583741

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ACCESSION BH583741

VERSION GI:17836198

KEYWORDS GSS

ORGANISM Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Brassica.

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AUTHORS

TITLE Whole genome shotgun sequencing of *Brassica oleracea*

JOURNAL Unpublished

COMMENT Contact: Chris Town

BASE COUNT 25 Soares and M. Fatima Bonaldo. "
ORIGIN 23 a 23 c 25 g 30 t

Query Match 52.6%; Score 10; DB 9; Length 103;
Best Local Similarity 52.6%; Pred. No. 2.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
| | | | | | | | | | | | | | | | | |
Db 55 CCAATTCAATCGGACCG 37

Search completed: December 4, 2003, 09:57:25
Job time : 2150 secs

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GenCore version 5.1.6
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model
Run on: December 4, 2003, 05:16:13 ; Search time 1492 Seconds
Title: US-09-606-804-1
Perfect score: 19
Sequence: 1 ccaatnnnnnnccacg 19
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 288871 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : GenEmpl:
1: gb:ba:
2: gb:htg:
3: gb:in:
4: gb:om:
5: gb:ov:
6: gb:pat:
7: gb:Dh:
8: gb:pl:
9: gb:pr:
10: gb:ro:
11: gb:sts:
12: gb:sy:
13: gb:un:
14: gb:vi:
15: em:ba:
16: em:fun:
17: em:hum:
18: em:in:
19: em:mu:
20: em:om:
21: em:or:
22: em:ov:
23: em:pat:
24: em:ph:
25: em:p1:
26: em:ro:
27: em:sts:
28: em:un:
29: em:vi:
30: em:htg:hum:
31: em:htg:inv:
32: em:htg:other:
33: em:htg:mus:
34: em:htg:pln:
35: em:hex:rod:
36: em:htg:man:
37: em:htg:vrt:
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39: em:htgo:hum:
40: em:htgo:mus:
41: em:htgo:other:

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1	10	52.6	19	AR274677 Sequence AX275341
2	10	52.6	19	BD016693 Method fo E28797
3	10	52.6	19	E28797 Endoplasmic
4	10	52.6	19	E28801 Endoplasmic
5	10	52.6	19	E28802 Endoplasmic
6	10	52.6	19	E28803 Endoplasmic
7	10	52.6	19	E28804 Endoplasmic
8	10	52.6	19	E28805 Endoplasmic
9	10	52.6	19	E28806 Endoplasmic
10	10	52.6	19	E28807 Endoplasmic
11	10	52.6	19	E28808 Endoplasmic
12	10	52.6	19	E28809 Endoplasmic
13	10	52.6	19	E28810 Endoplasmic
14	10	52.6	19	E44202 Endoplasmic
15	10	52.6	19	E44206 Endoplasmic
16	10	52.6	19	E44207 Endoplasmic
17	10	52.6	19	E44208 Endoplasmic
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19	10	52.6	19	E44210 Endoplasmic
20	10	52.6	19	E44211 Endoplasmic
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23	10	52.6	19	E44214 Endoplasmic
C	24	10	52.6	AX44732 Sequence
C	25	10	52.6	AX44733 Sequence
C	26	10	52.6	E44224
C	27	10	52.6	BD180759 Array of M10797 Human ade
C	28	10	52.6	HUMCC3A02
C	29	10	52.6	AF479941 Saccharom
C	30	10	52.6	AX343726 Sequence
C	31	10	52.6	AJ524636 Arabidops
C	32	10	52.6	E28800 Endoplasmic
C	33	10	52.6	E44205 Endoplasmic
C	34	10	52.6	AF271990 Human ade
C	35	10	52.6	AX343728 Sequence
C	36	10	52.6	AJ5233697 Arabidops
C	37	10	52.6	ATH53697
C	38	10	52.6	E28806 Arabidops
C	39	10	52.6	AX033516 Sequence
C	40	10	52.6	AY203001 Arabidops
C	41	10	52.6	AX033504 Sequence
C	42	10	52.6	DI0339S05
C	43	10	52.6	D10339S05
C	44	10	52.6	AX033508 Sequence

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
1	AR274677	Sequence 1 from patent US 6506600.	AR274677	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 19)	Hermanoff, P.L., Mane, M. and Liu, Y.	Secreting products from skin by adeno-associated virus (AAV) gene transfer	Patent: US 6506600-A 1 14-JAN-2003;
			AR274677							
			AR274677							
			AR274677							
			AR274677.1							

Pred. No. is the number of results predicted by chance to have a

FEATURES source	Location/Qualifiers 1..19 /organism="unknown"	PC (C12N15/00,C12R1:91) Description of Artificial Sequence:The sequence as shown in CC SEQ ID NO: 2 is ERSE consensus sequence.
BASE COUNT ORIGIN	3 a 5 c 1 g 1 t 9 others	CC n is A or C or G or T. Key Location/Qualifiers
Query Match Best Local Similarity Matches	52.6%; Score 10; DB 6; Length 19; 100.0%; Pred. No. 2.7e+04; 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES source 1..19 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32230"
Qy	1 CCAATNNNNNNCCACG 19	BASE COUNT 3 a 5 c 1 g 1 t 9 others
Db	1 CCAATNNNNNNCCACG 19	Query Match Best Local Similarity Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 2 AX275341	AX275341 19 bp LOCUS Sequence 1 from Patent WO0171018. DEFINITION ACCESSION AX275341 KEYWORDS . SOURCE unidentified ORGANISM unidentified unclassified.	PC (C12N15/00,C12R1:91) Description of Artificial Sequence: The sequence as shown in CC SEQ ID NO: 2 is ERSE consensus sequence. Key Location/Qualifiers
REFERENCE AUTHORS TITLE	Hermanat,P.L., Mane,M. and Liu,Y. Secreting products from skin by adeno-associated virus (aaV) gene transfer	FEATURES source 1..19 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644" /note:"glucose response element" 9 others
JOURNAL	PATENT: WO 0171018-A 1 27-SEP-2001; THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)	BASE COUNT 3 a 5 c 1 g 1 t 9 others
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Db	1 CCAATNNNNNNCCACG 19	Query Match Best Local Similarity Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 3 BD016693	BD016693 19 bp LOCUS Method for screening ORP150 expression regulatory substance. DEFINITION BD016693 VERSION BD016693.1 GI:22557869 KEYWORDS . SOURCE synthetic construct ORGANISM synthetic construct artificial sequences. 1. (bases 1 to 19) Akazawa,R., Kaneda,S., Yanagi,H. and Yura,T. Method for screening ORP150 expression regulatory substance Parent: JP 2001238699-A 2 04-SEP-2001; HSP RESEARCH INST INC OS Artificial Sequence PN JP 2001238699-A/2 PD 04-SEP-2001 PF 01-MAR-2000 JP 2000055384 PI RIKOU AKAZAWA, SUMIKO KANEDA, HIDEKI YANAGI, TAKASHI YURA PC C12Q1/68,A61K45/00,A61P1/04,A61P1/10,A61P9/10,A61P17/02,A61P25/ PC 28, A61P35/00,A61P37/00,C12N5/10,C12N15/09// (C12N5/10,C12R1:91), PC (C12N15/09,C12R1:91),C12N5/00,C12N15/00,(C12N5/00,C12R1:91), PC	PC (C12N15/00,C12R1:91) Description of Artificial Sequence: The sequence as shown in CC SEQ ID NO: 2 is ERSE consensus sequence. Key Location/Qualifiers
REFERENCE AUTHORS TITLE	Method for screening ORP150 expression regulatory substance Parent: JP 2001238699-A 2 04-SEP-2001; HSP RESEARCH INST INC OS Artificial Sequence PN JP 2001238699-A/2 PD 04-SEP-2001 PF 01-MAR-2000 JP 2000055384 PI RIKOU AKAZAWA, SUMIKO KANEDA, HIDEKI YANAGI, TAKASHI YURA PC C12Q1/68,A61K45/00,A61P1/04,A61P1/10,A61P9/10,A61P17/02,A61P25/ PC 28, A61P35/00,A61P37/00,C12N5/10,C12N15/09// (C12N5/10,C12R1:91), PC (C12N15/09,C12R1:91),C12N5/00,C12N15/00,(C12N5/00,C12R1:91), PC	FEATURES source 1..19 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"
JOURNAL		BASE COUNT 3 a 5 c 1 g 1 t 9 others
COMMENT		Query Match Best Local Similarity Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 5 E28801	E28801 19 bp LOCUS Endoplasmic reticulum stress-response regulatory element. DEFINITION ACCESSION E28801 VERSION E28801.1 GI:13020855	Query Match Best Local Similarity Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KEYWORDS	JP 1999243959-A/5.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Butheria; Primates;	
1 (bases 1 to 19)	
REFERENCE	
AUTHORS	Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE	Endoplasmic reticulum stress-response regulatory element
JOURNAL	Patent: JP 1999243959-A 5 14-SEP-1999;
COMMENT	HSP RESEARCH INST INC
OS	Homo sapiens (human)
PN	JP 1999243959-A/5
PD	14-SEP-1999
PR	04-MAR-1998 JP 1998052453
PI	HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PC	C12N15/09,A61K35/74,A61K38/00,A61K48/00,C12N15/00,
PC	A61K37/02
CC	Strandedness: Double;
CC	Topology: Linear;
Key	Location/Qualifiers
FT	enhancer 1..19.
FEATURES	Location/Qualifiers
source	1 .. 19 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
BASE COUNT	3 a 9 c 5 g 2 t
ORIGIN	
Query Match	52.6%; Score 10; DB 6; Length 19;
Best Local Similarity	52.6%; Pred. No. 2.7e+04;
Matches	0; Mismatches 9; Indels 0;
Qy	1 CCAATNNNNNNNNCCACG 19
Db	1 CCAATGGGGCTCCACG 19
RESULT 6	
E28802	
LOCUS	E228802 19 bp DNA linear PAT 18-JUN-2001
DEFINITION	Endoplasmic reticulum stress-response regulatory element.
ACCESSION	
VERSION	E28802.1 GI:13020856
KEYWORDS	JP 1999243959-A/6.
SOURCE	Mus sp.
ORGANISM	Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 19)	
REFERENCE	
AUTHORS	Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE	Endoplasmic reticulum stress-response regulatory element
JOURNAL	Patent: JP 1999243959-A 6 14-SEP-1999;
COMMENT	HSP RESEARCH INST INC
OS	Mus sp. (mouse)
PN	JP 1999243959-A/6
PD	14-SEP-1999
PR	04-MAR-1998 JP 1998052453
PI	HIDEO YOSHIDA,HIDEKI YANAGI,TAKASHI YURA
PC	C12N15/09,A61K35/74,A61K38/00,A61K48/00,C12N15/00,
PC	A61K37/02
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CC	Topology: Linear;
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Query Match	52.6%; Score 10; DB 6; Length 19;
Best Local Similarity	52.6%; Pred. No. 2.7e+04;
Matches	0; Mismatches 9; Indels 0;
Qy	1 CCAATNNNNNNNNCCACG 19
Db	1 CCAATGGGGCTCCACG 19
RESULT 8	
E28804	
LOCUS	E228804 19 bp DNA linear PAT 18-JUN-2001
DEFINITION	Endoplasmic reticulum stress-response regulatory element.
ACCESSION	
VERSION	E28804.1 GI:13020856
KEYWORDS	JP 1999243959-A/8
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
1 (bases 1 to 19)	
REFERENCE	
AUTHORS	Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE	Endoplasmic reticulum stress-response regulatory element
JOURNAL	Patent: JP 1999243959-A 8 14-SEP-1999;
COMMENT	HSP RESEARCH INST INC
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BASE COUNT	4 a 8 c 5 g 2 t

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	PN	JP 199243059-A/8						
	ED	14-SEP-1999						
	PF	-04-MAR-1998 JP 1998052453						
	PR	HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA						
	PI	C12N15/09, A61K35/74, A61K38/00, A61K48/00, C12N15/00,						
	PC	A61K37/02						
	CC	Strandedness: Double;						
	CC	Topology: Linear;						
	CC	Key enhancer	Location/Qualifiers					
	CC	1..19	/organism="Homo sapiens"					
	CC	/db_xref="taxon:9606"						
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BASE COUNT	ORIGIN							
Query Match		52.6%;	Score 10;	DB 6;	Length 19;			
Best Local Similarity		52.6%;	Pred. No. 2.7e+04;	9;	Indels 0;	Gaps 0;		
Matches		10;	Conservative 0;	Mismatches 9;				
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Db	1							
	1	CCAATCGCCGCCGACCAACG 19						
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LOCUS	E28805	Endoplasmic reticulum stress-response regulatory element.						
DEFINITION	E28805							
VERSION	E28805.1	GI:13020859						
REFERENCE	Qy	JP 199243059-A/9.						
AUTHORS	PI	HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA						
TITLE	PC	C12N15/09 A61K35/74, A61K38/00, A61K48/00, C12N15/00,						
JOURNAL	PC	A61K37/02						
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ORGANISM	CC	Topology: Linear;						
	CC	Key enhancer	Location/Qualifiers					
	CC	1..19	/organism="Homo sapiens"					
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FEATURES	source	6 a 6 c 6 g 1 t						
BASE COUNT	ORIGIN							
Query Match		52.6%;	Score 10;	DB 6;	Length 19;			
Best Local Similarity		52.6%;	Pred. No. 2.7e+04;	9;	Indels 0;	Gaps 0;		
Matches		10;	Conservative 0;	Mismatches 9;				
Qy	1	CCAATNNNNNNNNCCACG 19						
Db	1							
	1	CCAATGGGAGGCACACG 19						
RESULT 11	E28807	19 bp	DNA	linear	PAT 18-JUN-2001			
LOCUS	E28807	Endoplasmic reticulum stress-response regulatory element.						
DEFINITION	E28807							
VERSION	E28807.1	GI:13020861						
REFERENCE	Qy	JP 199243059-A 11 14-SEP-1999;						
AUTHORS	PI	Gallus sp.						
TITLE	PC	Gallus sp. (chicken)						
JOURNAL	PC	JP 199243059-A/9						
SOURCE	CC	Strandedness: Double;						
ORGANISM	CC	Topology: Linear;						
	CC	Key enhancer	Location/Qualifiers					
	CC	1..19	/organism="Gallus sp."					
	CC	/mol_type="genomic DNA"						
	CC	/db_xref="taxon:9036"						
FEATURES	source	5 a 7 c 6 g 1 t						
BASE COUNT	ORIGIN							
Query Match		52.6%;	Score 10;	DB 6;	Length 19;			
Best Local Similarity		52.6%;	Pred. No. 2.7e+04;	9;	Indels 0;	Gaps 0;		
Matches		10;	Conservative 0;	Mismatches 9;				
Qy	1	CCAATNNNNNNNNCCACG 19						
Db	1							

Query Match 52.6%; Score 10; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.7e+04;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Features source 1.19
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Qy	1	CCAAATNNNNNNNNCCAGC 19
Db	1	CCAAATNNNNNNNNCCAGC 19

RESULT 15

E44206	E44206	19 bp	DNA linear	PAT 31-JAN-2002
LOCUS	Endoplasmic reticulum stress transcription factor.			
DEFINITION				
ACCESSION	E44206			
VERSION	E44206.1			
KEYWORDS	GI:19633459			
SOURCE	JP 2001054391-A/5.			
ORGANISM	Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 19)			
AUTHORS	Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.			
TITLE	Endoplasmic reticulum stress transcription factor			
JOURNAL	Patent: JP 2001054391-A 5 27-FEB-2001;			
HSP RESEARCH INST INC				
COMMENT	OS Homo sapiens (human)			
PN	JP 2001054391-A/5			
PD	27-FEB-2001			
PF	11-NOV-1999			
PR	JP 1999321743			
PI	KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI			
TAKASHI YURA				
PC	C12N15/09, C12P21/02 // (C12N15/09, C12R1:91), C12N15/00, (C12N15/00, PC			
C12R1:91)				
CC				
FH	Key	Location/Qualifiers		
FT	source	1.19	/organism='Homo sapiens (human)'	
FEATURES	source	1.19		
BASE COUNT	3 a 9 c 5 g 2 t			
ORIGIN				
Qy	1	CCAAATNNNNNNNNCCAGC 19		
Db	1	CCAAATGGGCTCCACG 19		

Search completed: December 4, 2003, 07:13:02
 Job time : 1495 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 04:27:16 ; Search time 256 Seconds

(without alignments)

200.349 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19

Sequence: 1 ccaatnnnnnnccacg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9 10 52.6 19 20 AAZ25639
 10 10 52.6 19 20 AAZ25640
 11 10 52.6 19 21 AAA2570
 12 10 52.6 19 21 AAA2571
 13 10 52.6 19 21 AAA2572
 14 10 52.6 19 21 AAA2573
 15 10 52.6 19 21 AAA2574
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 17 10 52.6 19 21 AAA2576
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 19 10 52.6 19 21 AAA2578
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 21 10 52.6 19 22 AAQ10001
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 C 24 10 52.6 24 ABQ0200
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 C 26 10 52.6 24 ABQ04439
 C 27 10 52.6 24 ABQ1685
 C 28 10 52.6 24 ABQ1726
 C 29 10 52.6 25 AAV4529
 C 30 10 52.6 25 ABQ1221
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 C 32 10 52.6 28 AAA28597
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 C 34 10 52.6 29 AAA2602
 C 35 10 52.6 30 AAA28598
 C 36 10 52.6 33 AAA28569
 C 37 10 52.6 50 ABZ0658
 C 38 10 52.6 112 AB141923
 39 10 52.6 122 AA25560
 40 10 52.6 122 AAA28566
 41 10 52.6 123 AB180984
 42 10 52.6 126 AA171906
 43 10 52.6 127 ABL1924
 44 10 52.6 143 AAA71907
 C 45 10 52.6 145 AAF67488

ALIGNMENTS

RESULT 1
 AAZ25631
 ID AAZ25631 standard; DNA; 19 BP.
 XX
 AC
 AAZ25631;
 XX
 DT 23-DEC-1999 (first entry)
 XX
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:1.
 XX
 KW Endoplasmic reticulum; ER; stress competence; control element;
 KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX
 Homo sapiens.
 XX
 OS Homo sapiens.
 XX
 PN JP11243959-A.
 XX
 PD 14-SEP-1999.
 XX
 PF 04-MAR-1998;
 XX
 PR 04-MAR-1998;
 XX
 PA (HSPK-) HSP KENKYUSHO KK.
 XX
 DR WP1; 1999-603708/52.
 PT New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer
 PT cells

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	52.6	19	20 AAZ25631	Endoplasmic reticulum
2	10	52.6	19	20 AAZ25632	Endoplasmic reticulum
3	10	52.6	19	20 AAZ25633	Endoplasmic reticulum
4	10	52.6	19	20 AAZ25634	Endoplasmic reticulum
5	10	52.6	19	20 AAZ25635	Endoplasmic reticulum
6	10	52.6	19	20 AAZ25636	Endoplasmic reticulum
7	10	52.6	19	20 AAZ25637	Endoplasmic reticulum
8	10	52.6	19	20 AAZ25638	Endoplasmic reticulum

XX Claim 1; Page 10; 25pp; Japanese.

XX Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;

CC Query Match 52.6%; Score 10; DB 20; Length 19;
CC Best Local Similarity 52.6%; Pred. No. 1.8e+03;
CC Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

CC Qy 1 CCAATNNNNNNNNCCACG 19
CC |||||
CC Db 1 CCAATGGGGCCCTCACCG 19
CC |||||

RESULT 3
AAZ25633
ID AAZ25633 standard; DNA; 19 BP.

XX Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;

CC Query Match 52.6%; Score 10; DB 20; Length 19;
CC Best Local Similarity 100.0%; Pred. No. 1.8e+03;
CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 CCAATNNNNNNNNCCACG 19
CC |||||
CC Db 1 CCAATNNNNNNNNCCACG 19
CC |||||

RESULT 2
AAZ25632
ID AAZ25632 standard; DNA; 19 BP.

XX AC AAZ25632;
XX DT 23-DEC-1999 (first entry)

XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:5.
XX KW Endoplasmic reticulum; ER; stress competence; control element;
XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
XX KW cystic fibrosis; ds.
XX OS Mus sp.
XX PN JP11243959-A.
XX PD 14-SEP-1999.
XX PR 04-MAR-1998;
XX PA 98JP-0052453.
XX DR WPI; 1999-603708/52.
XX PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
cells

XX PS Example 1; Fig 3; 25pp; Japanese.

XX CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNN NNNNCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC antibody formation. AAZ25632 to AAZ25657 represent elements used in
CC an example from the present invention.

XX SQ Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;

CC Query Match 52.6%; Score 10; DB 20; Length 19;
CC Best Local Similarity 52.6%; Pred. No. 1.8e+03;
CC Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

CC Qy 1 CCAATNNNNNNNNCCACG 19
CC |||||
CC Db 1 CCAATGGGGCCCTCACCG 19
CC |||||

RESULT 4
AAZ25634

ID AAZ25634 standard; DNA; 19 BP.
 XX
 AC AAZ25634;
 XX DT 23-DEC-1999 (First entry)
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:7.
 XX
 Endoplasmic reticulum; ER; stress competence; control element;
 KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX OS Rattus sp.
 PN JP11243959-A.
 XX PD 14-SEP-1999.
 XX PF 04-MAR-1998;
 XX PR 04-MAR-1998;
 XX PA (HSPK-) HSP KENKYUSHO KK.
 XX DR WPI: 1999-603708/52.
 XX PT New control element for stress competence of endoplasmic reticulum - useful for inhibition or growth and induction of apoptosis in cancer cells.
 XX PT Example 1; Fig 3; 25pp; Japanese.
 XX CC The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNN NNNNCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of antibody formation. AAZ25632 to AAZ25637 represent elements used in an example from the present invention.
 XX SQ Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
 CC Query Match 52.6%; Score 10; DB 20; Length 19;
 CC Best Local Similarity 52.6%; Pred. No. 1.4e+03;
 CC Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 CC Qy 1 CCAATNNNNNNNNNCCACCG 19
 CC Db 1 CCAATGGGGCTCCACCG 19
 RESULT 6
 ID AAZ25636
 DE AAZ25636 standard; DNA; 19 BP.
 XX AC AAZ25636;
 XX DT 23-DEC-1999 (first entry)
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:9.
 XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX OS Gallus sp.
 XX JP11243959-A.
 XX PD 14-SEP-1999.
 XX PR 04-MAR-1998;
 XX PA (HSPK-) HSP KENKYUSHO KK.
 XX DR WPI: 1999-603708/52.
 XX PT New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer cells.

RESULT 9
 AA225639 standard; DNA; 19 BP.
 ID AA225639;
 XX AC
 XX DT 23-DEC-1999 (first entry)
 XX DE Endoplasmic reticulum stress competence control element SEQ ID NO:12.
 XX KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 XX cystic fibrosis; ds.
 OS Homo sapiens.
 XX PN JP11241959-A.
 XX PD 14-SEP-1999.
 XX PF 04-MAR-1998; 98JP-0052453.
 XX PA (HSPK-) HSP KENKYUSHO KK.
 XX DR WPI; 1999-603708/52.
 XX PS Example 1; Fig 3; 25pp; Japanese.

The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNN NNNNCACG (ERSB); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of antibody formation. AA225632 to AA225657 represent elements used in an example from the present invention.

CC Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
 CC Query Match 52.6%; Score 10; DB 20; Length 19;
 CC Best Local Similarity 52.6%; Pred. No. 1.8e+03;
 CC Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 CC Qy 1 CCAATNNNNNNNNNNCCACG 19
 CC Db 1 CCAATGGGTGACCAACG 19
 XX RESULT 11
 XX AAA28570 AAA28570 standard; DNA; 19 BP.
 XX ID AAA28570;
 XX AC AAA28570;
 XX DT 29-AUG-2000 (first entry)
 XX DE GRP78 promoter ERSB1-like sequence.
 XX KW Endoplasmic reticulum; stress; ER; transcription factor;
 XX KW transcription regulatory element; ERSB; bZIP; chaperone; treatment;
 XX KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
 XX KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
 XX KW gene expression; GRP; glucose regulated protein; promoter; 86.
 XX OS Homo sapiens.
 XX PN WO200029429-A2.
 XX DT 25-MAY-2000.
 XX PA 12-NOV-1999; 99WO-JP06305.
 XX PR 13-NOV-1999; 98JP-0324227.
 XX PR 09-JUN-1999; 99JP-0163112.

XX Mu8 sp.
 XX OS
 XX PN JP11241959-A.
 XX XX
 XX PD 14-SEP-1999.
 XX XX
 XX PF 04-MAR-1998; 98JP-0052453.
 XX XX
 XX PR 04-MAR-1998; 98JP-0052453.
 XX PA (HSPK-) HSP KENKYUSHO KK.
 XX XX
 XX DR WPI; 1999-603708/52.
 XX PS New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer cells.
 XX XX
 XX PS Example 1; Fig 3; 25pp; Japanese.
 XX CC The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNN NNNNCACG (ERSB); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of antibody formation. AA225632 to AA225657 represent elements used in an example from the present invention.

SQ Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
 SQ Query Match 52.6%; Score 10; DB 20; Length 19;
 SQ Best Local Similarity 52.6%; Pred. No. 1.8e+03;
 SQ Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 SQ Qy 1 CCAATNNNNNNNNCCACG 19
 SQ Db 1 CCAATGGGTGACCAACG 19
 XX RESULT 11
 XX AAA28570 AAA28570 standard; DNA; 19 BP.
 XX ID AAA28570;
 XX AC AAA28570;
 XX DT 29-AUG-2000 (first entry)
 XX DE GRP78 promoter ERSB1-like sequence.
 XX KW Endoplasmic reticulum; stress; ER; transcription factor;
 XX KW transcription regulatory element; ERSB; bZIP; chaperone; treatment;
 XX KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
 XX KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
 XX KW gene expression; GRP; glucose regulated protein; promoter; 86.
 XX OS Homo sapiens.
 XX PN WO200029429-A2.
 XX DT 25-MAY-2000.
 XX PA 12-NOV-1999; 99WO-JP06305.
 XX PR 13-NOV-1999; 98JP-0324227.
 XX PR 09-JUN-1999; 99JP-0163112.

PA (HSPR-) HSP RES INST INC.
 XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
 PI XX WPI; 2000-387736/33.

PT New endoplasmic reticulum stress transcription factor (known as bZIP)
 PT for controlling expression of endoplasmic reticulum chaperone, useful
 PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 PT diseases, wounds and ulcers
 XX

PS Example 1; Fig 3; 157pp; English.

PT An endoplasmic reticulum stress transcription factor (bZIP)
 PT for controlling expression of endoplasmic reticulum chaperone, useful
 PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 PT diseases, wounds and ulcers
 XX

PS Example 1; Fig 3; 157pp; English.

CC An endoplasmic reticulum stress transcription inducing activity exhibited by an
 CC element (ERSE) capable of regulating transcription induced by an
 CC element (ERSE) can be used in a method for controlling expression of
 CC an endoplasmic reticulum chaperone. The method comprises expressing
 CC bZIP. The method can be used for expression of a foreign protein by
 CC positively regulating expression of an endoplasmic reticulum
 CC chaperone gene. bZIP is useful for controlling the expression of an
 CC endoplasmic reticulum chaperone either positively or negatively in
 CC cells and therefore is useful for treatment or prophylaxis of
 CC cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 CC wounds and ulcers. bZIP also maintains the correct conformation of
 CC the endoplasmic reticulum chaperone and thereby increases the
 CC expression of a foreign protein. This sequence taken from the
 CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
 CC sequence.
 XX

SQ Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;

Query Match Score 10; DB 21; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCAGC 19
 ||||| | | | |
 Db 1 CCAATGGGGCTCCACG 19

RESULT 13
 AAA28572
 ID AAA28572 standard; DNA; 19 BP.
 XX
 AC AAA28572;
 XX
 DT 29-AUG-2000 (first entry)
 DE GRP78 promoter ERSE1-like sequence.
 KW Endoplasmic reticulum; stress; ER; transcription factor;
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 KW prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
 KW cystic fibrosis; ulcer; gene therapy; recombinant gene; rat;
 KW gene expression; GRP; glucose regulated protein; promoter; ss.
 OS Rattus rattus.
 XX
 PN WO200029429-A2.
 PR 13-NOV-1998;
 PD 25-MAY-2000.
 XX
 PF 09-JUN-1999; 99WO-JP06305.
 XX
 PA (HSPR-) HSP RES INST INC.
 XX
 PR 13-NOV-1998; 98JP-034227.
 PR 09-JUN-1999; 99JP-0163112.
 PA (HSPR-) HSP RES INST INC.
 XX
 PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
 XX
 DR 2000-387736/33.

PT New endoplasmic reticulum stress transcription factor (known as bZIP)
 PT for controlling expression of endoplasmic reticulum chaperone, useful
 PT for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 PT diseases, wounds and ulcers
 XX

PS Example 1; Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of an endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP78 contains an ERSE like sequence.

XX Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
 Query Match 52.6%; Score 10; DB 21; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 |||||
 Db 1 CCAATGGGGCTCCACAG 19

RESULT 14
 AAA28573 standard; DNA; 19 BP.
 ID AAA28573 XX
 AC AAA28573 XX
 DE GRP94 promoter ERSE1-like sequence. DT 29-AUG-2000 (first entry)
 KW Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken; gene expression; GRP; glucose regulated protein; promoter; ss. OS Gallus domesticus.
 XX WO200029429-A2. PN 99WO-JP030305.
 XX 13-NOV-1998; PR 98JP-032227.
 XX 09-JUN-1999; PR 99JP-016112.
 DE (HSPR-) HSP RES INST INC. PA (HSPR-) HSP RES INST INC.
 KW Haze K, Yoshida H, Mori K, Yanagi H, Yura T; PI
 XX 12-MAY-2000. PD 25-MAY-2000.
 XX 12-NOV-1999; PR 99WO-JP06305.
 XX 13-NOV-1998; PR 98JP-0324227.
 XX 09-JUN-1999; PR 99JP-0163112.
 PA (HSPR-) HSP RES INST INC. DR WPI: 2000-387736/33.
 XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T; PT New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic diseases, wounds and ulcers. PT Example 1; Fig 3; 157pp; English.

XX WPI: 2000-387736/33. PS New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic diseases, wounds and ulcers. PT Example 1; Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of the endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of

XX positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of an endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP94 contains an ERSE like sequence.

XX Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
 SQ Query Match 52.6%; Score 10; DB 21; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.8e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 |||||
 Db 1 CCAATGGGGCTCCACAG 19

RESULT 15
 AAA28574 standard; DNA; 19 BP.
 ID AAA28574 XX
 AC AAA28574 XX
 DE GRP94 promoter ERSE1-like sequence. DT 29-AUG-2000 (first entry)
 KW Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken; gene expression; GRP; glucose regulated protein; promoter; ss. OS Gallus domesticus.
 XX WO200029429-A2. PN 99WO-JP030305.
 XX 13-NOV-1998; PR 98JP-032227.
 XX 09-JUN-1999; PR 99JP-016112.
 DE (HSPR-) HSP RES INST INC. PA (HSPR-) HSP RES INST INC.
 KW Haze K, Yoshida H, Mori K, Yanagi H, Yura T; PI
 XX 12-MAY-2000. PD 25-MAY-2000.
 XX 12-NOV-1999; PR 99WO-JP06305.
 XX 13-NOV-1998; PR 98JP-0324227.
 XX 09-JUN-1999; PR 99JP-0163112.
 PA (HSPR-) HSP RES INST INC. DR WPI: 2000-387736/33.
 XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T; PT New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic diseases, wounds and ulcers. PT Example 1; Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of the endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of

CC the endoplasmic reticulum chaperone and thereby increases the
CC expression of a foreign protein. This sequence taken from the
CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
CC sequence.

XX Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
SQ Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e-03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
| | | | | | | | | |
1 CCAATGGAGGCCACACG 19
Db

Search completed: December 4, 2003, 06:47:54
Job time : 257 secs

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OM nucleic - nucleic search, using sw model

Run on: December 4, 2003, 06:00:59 ; Search time 74 Seconds
 (without alignments)
 113,328 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19

Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 4 summaries

Database : Issued_Patents_NA.*

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 2: /cgn2_6/podata/2/ina/5B_COMB.seq; *
 3: /cgn2_6/podata/2/ina/6A_COMB.seq; *
 4: /cgn2_6/podata/2/ina/6B_COMB.seq; *
 5: /cgn2_6/podata/2/ina/PCUTUS_COMB.seq; *
 6: /cgn2_6/podata/2/ina/backfile1.seq; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	52.6	19	4	US-09-813-937-1
2	10	52.6	205	4	US-09-313-294A-1696
3	10	52.6	261	4	US-09-389-581-206
4	10	52.6	261	4	US-09-620-405B-206
5	10	52.6	261	4	US-09-339-338-206
6	10	52.6	261	4	US-09-433-326B-206
7	10	52.6	261	4	US-09-604-287A-206
8	10	52.6	270	4	US-09-313-294A-890
9	10	52.6	272	1	US-08-248-874-36
10	10	52.6	272	3	US-08-756-849-36
11	10	52.6	282	4	US-09-252-991A-987
12	10	52.6	285	4	US-09-252-991A-0
13	10	52.6	296	2	US-08-716-942-20
14	10	52.6	296	4	US-09-130-337A-20
15	10	52.6	300	4	US-09-313-294A-348
16	10	52.6	360	6	5196523-1
17	10	52.6	387	3	US-08-804-372A-23
18	10	52.6	392	4	US-09-404-879A-72
19	10	52.6	399	6	5196523-23
20	10	52.6	421	6	5196523-22
21	10	52.6	424	1	US-08-609-657-15
22	10	52.6	432	4	US-09-252-991A-9959
23	10	52.6	457	4	US-09-702-705-861
24	10	52.6	457	4	US-09-736-457-861
25	10	52.6	467	3	US-09-257-584-8
26	10	52.6	511	4	US-09-702-705-1138
27	10	52.6	511	4	US-09-736-457-1138

ALIGNMENTS

RESULT 1

US-09-813-937-1
 ; Sequence 1, Application US/09813937
 ; Patent No. 6506600
 ; GENERAL INFORMATION:
 ; APPLICANT: HERMONAT, Paul L.
 ; LIU, Yong
 ; TITLE OF INVENTION: SECRETING PRODUCTS FROM SKIN BY ADENO-ASSOCIATED VIRUS (AAV) GEN
 ; FILE REFERENCE: 023533/01/16
 ; CURRENT APPLICATION NUMBER: US/09-332-149A-20
 ; PRIORITY FILING DATE: 2000-03-22
 ; PRIORITY APPLICATION NUMBER: US 60/191092
 ; NUMBER OF SEQ ID NOS: 4
 ; SEQ ID NO 1
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: glucose response element
 ; APPLICANT: MANE, Michael
 ; LIU, Yong
 ; TITLE OF INVENTION: SECRETING PRODUCTS FROM SKIN BY ADENO-ASSOCIATED VIRUS (AAV) GEN
 ; FILE REFERENCE: 023533/01/16
 ; CURRENT APPLICATION NUMBER: US/09-813-937-1
 ; PRIORITY FILING DATE: 2000-03-22
 ; PRIORITY APPLICATION NUMBER: US 60/191092
 ; NUMBER OF SEQ ID NOS: 4
 ; SEQ ID NO 1
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: glucose response element
 ; APPLICANT: MANE, Michael
 ; LIU, Yong
 ; LOCATION: (6) -(14)
 ; OTHER INFORMATION: "N" at positions 6 - 14 can be A, C, G or T
 ; Query Match Best Local Similarity 100.0%; Pred. No. 3 5e+02;
 ; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATNNNNNNNNNNNCACG 19
 Db 1 CCATNNNNNNNNNNNCACG 19

RESULT 2

US-09-313-294A-1696/c
 ; Sequence 1696, Application US/09313294A
 ; Patent No. 647612
 ; GENERAL INFORMATION:
 ; APPLICANT: Laligudi, Raghunath V.
 ; Ito, Laura Y.
 ; Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PI-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14

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; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1696
; LENGTH: 205
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551354H1
US-09-313-29A-1696

Query Match 52.6%; Score 10; DB 4; Length 205;
Best Local Similarity 52.6%; Pred. No. 5.2e+02; Mismatches 9; Indels 0; Gaps 0;
Matches 10; Conservative 0; Sequence 206; Application US/09339338A
Qy 1 CCAATNNNNNNNNCCACG 19
Db 122 CCAATCAGACAGACCACCG 104

RESULT 3
US-09-389-681-206
Sequence 206, Application US/09389681A
GENERAL INFORMATION:
APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C2
CURRENT APPLICATION NUMBER: US/09/339, 338A
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 315
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 206
LENGTH: 261
TYPE: DNA
ORGANISM: Homo sapiens
US-09-389-681-206

Query Match 52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02; Mismatches 9; Indels 0; Gaps 0;
Matches 10; Conservative 0; Sequence 206; Application US/09433826B
Qy 1 CCAATNNNNNNNNCCACG 19
Db 140 CCAATTCTCATCTCCACG 158

RESULT 4
US-09-420-405B-206
Sequence 206, Application US/09620405B
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C4
CURRENT APPLICATION NUMBER: US/09/433, 826B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 474
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 206
LENGTH: 261
TYPE: DNA
ORGANISM: Homo sapiens
US-09-420-405B-206

Query Match 52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02; Mismatches 9; Indels 0; Gaps 0;
Matches 10; Conservative 0; Sequence 206; Application US/0933826B
Qy 1 CCAATNNNNNNNNCCACG 19
Db 140 CCAATTCTCATCTCCACG 158

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RESULT 7
US-09-604-287A-206
; Sequence 890, Application US/09604287A
; Patent No. 6586572
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jianguchun
APPLICANT: Harlocher, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C7
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 1.0
SEQ ID NO: 206
LENGTH: 261
TYPE: DNA
ORGANISM: Homo sapiens
US-09-604-287A-206

Query Match 52.6%; Score 10; DB 4; Length 261;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 140 CCAATTCTTCATCTCCACG 158

RESULT 8
US-09-313-294A-890/C
; Sequence 890, Application US/09313294A
; Patent No. 6416212
GENERAL INFORMATION:
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313-294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO: 890
LENGTH: 270
TYPE: DNA
ORGANISM: Zea mays

FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700550018H1
NAME/KEY: unsure
LOCATION: 213-215, 218-221, 232-233, 236-237, 239-240, 242, 249, 251, 253, 261,
OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-890

Query Match 52.6%; Score 10; DB 4; Length 270;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 121 CCAATCAGACAGACCCACG 103

RESULT 9
US-08-248-474-36
; Sequence 36, Application US/08248474
; Patent No. 5612471

GENERAL INFORMATION:
APPLICANT: MCK. BIRD, David
APPLICANT: WILSON, Mark A.
TITLE OF INVENTION: NEEMATO-INDUCE GENES IN TOMATO
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0., Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,474
FILING DATE: 25-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-535
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9000
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Lycopersicon esculentum cv 'Rutgers Large
RED'
ORGANISM:
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..272
OTHER INFORMATION: / standard_name= "DB# 155"
US-08-248-474-36

Query Match 52.6%; Score 10; DB 1; Length 272;
Best Local Similarity 52.6%; Pred. No. 5.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 97 CCAATTATTTCACCG 115

RESULT 10
US-08-756-849-36
; Sequence 36, Application US/08756849
; Patent No. 6093810
GENERAL INFORMATION:
APPLICANT: Bird, David McK.
APPLICANT: Wilson, Mark A.
TITLE OF INVENTION: Nemato-Induced Genes in Tomato
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/756,849
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/248,474
 FILING DATE: 25-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bistian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 023070-053510US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEX/FAX: (415) 576-0100
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 272 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..272
 OTHER INFORMATION: /standard_name= "DB# 155"
 US - 08-756-849-36

RESULT 11
 Query Match 52.6%; Score 10; DB 3; Length 272;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 97 CCAATTATTTCACCG 115

US-09-252-991A-987
 Sequence 987, Application US/09252991A
 PATENT NO. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 10/7196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIOR APPLICATION NUMBER: 1999-02-18
 PRIOR FILING DATE: 1998-02-18
 PRIOR FILING DATE: 1998-02-18
 NUMBER OF SEQ ID NOS: 33142
 LENGTH: 282
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-987

Query Match 52.6%; Score 10; DB 4; Length 282;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 49 CCAATGCTGATCCCCACCG 67

RESULT 12
 US-09-252-991A-60
 Sequence 60, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 10/7196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR APPLICATION NUMBER: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; LENGTH: 285
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-60

Query Match 52.6%; Score 10; DB 4; Length 285;
 Best Local Similarity 52.6%; Pred. No. 5.4e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 224 CCAATGACCGATAACCG 242

RESULT 13
 US-08-716-942-20/c
 Sequence 20, Application US/08716942
 ; Patent No. 5849431
 GENERAL INFORMATION:
 ; APPLICANT: Terragen Diversity Inc.
 ; ADDRESS: Oppenheim & Larson
 ; CITY: Yorktown Heights
 ; STATE: NY USA
 ; ZIP: 10598-4412
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS 5.0
 ; SOFTWARE: Word Perfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/715,942
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/004,157
 ; FILING DATE: 20-Sep-95
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Marina T. Larson
 ; REGISTRATION NUMBER: 32,038
 ; REFERENCE/DOCKET NUMBER: TERR.P-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (914) 245-3252
 ; TELEFAX: (914) 962-4330
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 296
 ; TYPE: nucleic acid

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STRANDEDNESS: DOUBLE
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM:
FEATURE:
NAME/KEY: fragment of xylanase gene from degenerate primer
US-09-716-942-20
NAME/KEY: amplification of soil DNA

Query Match      52.6%; Score 10; DB 2; Length 296;
Best Local Similarity 52.6%; Pred. No. 5.5e+02; Length 300;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy   1 CCAATNNNNNNNNCCACG 19
     ||||| | | | | |
Db   217 CCAATGGTGTGGCCACG 199

RESULT 14
US-09-130-317A-20/C
Sequence 20, Application US/09130337A
GENERAL INFORMATION
APPLICANT: Redomski, CCA
APPLICANT: Seow, KT
APPLICANT: Warren, RAJ
APPLICANT: Yap, WH
TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIONS
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 993-3-004
CURRENT APPLICATION NUMBER: US/09/130,337A
CURRENT FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 08/716,942
PRIOR FILING DATE: 1996-09-20
PRIOR APPLICATION NUMBER: 60/004,157
PRIOR FILING DATE: 1995-09-22
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 20
LENGTH: 296
TYPE: DNA
ORGANISM: Unknown organism
FEATURE: OTHER INFORMATION: Description of unknown organism: soil microbe
US-09-130-337A-20

Query Match      52.6%; Score 10; DB 4; Length 296;
Best Local Similarity 52.6%; Pred. No. 5.5e+02; Length 300;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy   1 CCAATNNNNNNNNCCACG 19
     ||||| | | | | |
Db   217 CCAATGGTGTGGCCACG 199

RESULT 15
US-09-313-294A-7348/C
Sequence 7348, Application US/0913294A
PATENT NO. 6476212
GENERAL INFORMATION
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program

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Result No.	Score	Query	Match	Length	DB ID	Description
c 1	10	52.6	19	14	US-10-345-759-1	Sequence 1, Appl
c 2	10	52.6	24	11	US-09-940-185-207	Sequence 207, Appl
c 3	10	52.6	25	9	US-09-402-100-35	Sequence 35, Appl
c 4	10	52.6	25	11	US-09-945-185-4188	Sequence 4188, AP
c 5	10	52.6	100	10	US-09-960-73-1152	Sequence 1152, AP
c 6	10	52.6	123	10	US-09-867-701-3962	Sequence 3962, AP
c 7	10	52.6	136	12	US-09-922-4498-18	Sequence 18, Appl
c 8	10	52.6	136	12	US-09-922-4498-19	Sequence 19, Appl
c 9	10	52.6	142	12	US-09-922-4498-8	Sequence 8, Appl
c 10	10	52.6	143	12	US-09-922-4498-24	Sequence 24, Appl
c 11	10	52.6	149	12	US-09-922-4498-25	Sequence 25, Appl
c 12	10	52.6	150	12	US-09-922-4498-10	Sequence 10, Appl
c 13	10	52.6	167	14	US-10-001-883-5	Sequence 5, Appl
c 14	10	52.6	210	10	US-09-974-300-8096	Sequence 8096, AP
c 15	10	52.6	214	9	US-09-770-320-59	Sequence 59, Appl
c 16	10	52.6	214	9	US-09-910-689-59	Sequence 59, Appl

RESULT 2
US-09-940-185-207/c
Sequence 207, Application US/0940185
Publication No. US20030096239A1
APPLICANT: Gunderson, Kevin
APPLICANT: Chee, Mark
TITLE OF INVENTION: Probes and Decoder Oligonucleotides
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09/940,185
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 4768
SOFTWARE: Patentin version 3.1
SEQ ID NO: 207
LENGTH: 24
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-207

Query Match Score 10; DB 11; Length 24;
Best Local Similarity 52.6%; Pred. No. 4.2e+03; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 23 CCAATTACGTGACCAAG 5

RESULT 3
US-09-402-100-35/c
Sequence 35, Application US/09402100
GENERAL INFORMATION:
APPLICANT: Daewoong Pharmaceutical Co., LTD
APPLICANT: Kim, Byung-O
APPLICANT: Shin, Sung-Seup
APPLICANT: Yu, Young-Hyo
APPLICANT: Park, Myung-Hwan
APPLICANT: Choi, Deok-Joon
APPLICANT: Jung, Hyung-Jin
TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Helicobacter pylori
FILE REFERENCE: 0136/0G140
CURRENT APPLICATION NUMBER: US/09/402,100
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: KR 97-11950
EARLIER FILING DATE: 1997-03-31
EARLIER APPLICATION NUMBER: KR 97-11951
EARLIER FILING DATE: 1997-03-31
SOFTWARE: Patentin version 3.0
SEQ ID NO: 35
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: ()
OTHER INFORMATION: Oligonucleotide
US-09-402-100-35

Query Match Score 10; DB 9; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 97 CCATCATTTCCATCCACG 79

RESULT 4
US-09-940-185-4188/c
Sequence 4188, Application US/09940185
Publication No. US20030096239A1
GENERAL INFORMATION:
APPLICANT: Gunderson, Kevin
APPLICANT: Chee, Mark
TITLE OF INVENTION: Probes and Decoder Oligonucleotides
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09/940,185
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/228,854
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 4768
SOFTWARE: Patentin version 3.1
SEQ ID NO: 4188
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-4188

Query Match Score 10; DB 11; Length 25;
Best Local Similarity 52.6%; Pred. No. 4.2e+03; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
Db 24 CCAATTACGTGACCAAG 6

RESULT 5
US-09-969-373-1152/c
Sequence 1152, Application US/09969373
Patent No. US2004133852A1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Haug, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10/52679/A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4553
SEQ ID NO: 1152
LENGTH: 100
TYPE: DNA
ORGANISM: Glycine max
US-09-969-373-1152

Query Match Score 10; DB 10; Length 100;
Best Local Similarity 52.6%; Pred. No. 4.e+03; Indels 0; Gaps 0;

Qy 1 CCATATNNNNNNCCACG 19
Db 97 CCATCATTTCCATCCACG 79

RESULT 6
US-09-867-701-3962
Sequence 3962, Application US/09867701

Qy 1 CCAATNNNNNNNNCCACG 19
Db 97 CCATCATTTCCATCCACG 79

Patent No. US20020132237A1
 GENERAL INFORMATION:
 APPLICANT: Aglate, Paul A.
 APPLICANT: Jones, Robert L.
 APPLICANT: Harlocker, Susan L.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 FILE REFERENCE: 21.0121.497
 CURRENT APPLICATION NUMBER: US/09/867.701
 CURRENT FILING DATE: 2001-08-29
 NUMBER OF SEQ ID NOS: 10912
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 3962
 LENGTH: 123
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-867-701-3962

RESULT 7
 US-09-922-449B-18
 / Sequence 18, Application US/09922449B
 / Publication No. US20030148278A1
 GENERAL INFORMATION:
 / APPLICANT: Bioinside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting mbH
 / APPLICANT: mbH
 / TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified organisms in foodstuff by means of fluorescent-coupled PCR
 / FILE REFERENCE: 101215-68
 CURRENT APPLICATION NUMBER: US/09/922.449B
 CURRENT FILING DATE: 2001-08-03
 PRIORITY APPLICATION NUMBER: PCT/EP00/009835
 PRIORITY FILING DATE: 2000-02-07
 PRIORITY APPLICATION NUMBER: DE 199 06 169.6
 PRIORITY FILING DATE: 1999-02-08
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 18
 LENGTH: 136
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the Bt-176
 OTHER INFORMATION: maize gen
 US-09-922-449B-18

Query Match 52.6%; Score 10; DB 12; Length 136;
 Best Local Similarity 52.6%; Pred. No. 5.e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 27 CCATTTTCGGTCCACAG 45

RESULT 8
 US-09-922-449B-19
 / Sequence 19, Application US/09922449B
 / Publication No. US20030148278A1
 GENERAL INFORMATION:
 / APPLICANT: Bioinside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting mbH
 / APPLICANT: mbH
 / TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified organisms in foodstuff by means of fluorescent-coupled PCR
 / FILE REFERENCE: 101215-68
 CURRENT APPLICATION NUMBER: US/09/922.449B
 CURRENT FILING DATE: 2001-08-03

Query Match 52.6%; Score 10; DB 12; Length 142;
 Best Local Similarity 52.6%; Pred. No. 5.e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 31 CCATTTTCGGTCCACAG 49

RESULT 9
 US-09-922-449B-8
 / Sequence 8, Application US/09922449B
 / Publication No. US20030148278A1
 GENERAL INFORMATION:
 / APPLICANT: Bioinside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting mbH
 / APPLICANT: mbH
 / TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified organisms in foodstuff by means of fluorescent-coupled PCR
 / FILE REFERENCE: 101215-68
 CURRENT APPLICATION NUMBER: US/09/922.449B
 CURRENT FILING DATE: 2001-08-03
 PRIORITY APPLICATION NUMBER: PCT/EP00/009835
 PRIORITY FILING DATE: 2000-02-07
 PRIORITY APPLICATION NUMBER: DE 199 06 169.6
 PRIORITY FILING DATE: 1999-02-08
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 8
 LENGTH: 142
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the RRS 9
 OTHER INFORMATION: maize gen
 US-09-922-449B-8

Query Match 52.6%; Score 10; DB 12; Length 142;
 Best Local Similarity 52.6%; Pred. No. 5.e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCACG 19
 Db 31 CCATTTTCGGTCCACAG 49

RESULT 10
 US-09-922-449B-24
 / Sequence 24, Application US/09922449B
 / Publication No. US20030148278A1
 GENERAL INFORMATION:
 / APPLICANT: Bioinside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting mbH
 / APPLICANT: mbH
 / TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified organisms in foodstuff by means of fluorescent-coupled PCR
 / FILE REFERENCE: 101215-68
 CURRENT APPLICATION NUMBER: US/09/922.449B
 CURRENT FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: PCT/EP00/009835
 PRIOR FILING DATE: 2000-02-07
 PRIOR APPLICATION NUMBER: DE 199 06 169.6
 PRIOR FILING DATE: 1999-02-08
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 24
 LENGTH: 143
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: target IAC DNA for the RRS gene
 US-09-922-449B-24

Query Match 52.6%; Score 10; DB 12; Length 143;
 Best Local Similarity 52.6%; Pred. No. 5.1e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 31 CCAATTTCGGCTCCACG 49

RESULT 11

US-09-922-449B-25
 Sequence 25, Application US/09922449B
 Publication No. US20030148278A1
 GENERAL INFORMATION:
 APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting mbH
 TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified foodstuff by means of fluorescent-coupled PCR
 FILE REFERENCE: 101215-68
 CURRENT APPLICATION NUMBER: US/09/922,4493
 CURRENT FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: PCT/EP00/009835
 PRIOR FILING DATE: 2000-02-07
 PRIOR APPLICATION NUMBER: DE 199 06 169.6
 PRIOR FILING DATE: 1999-02-08
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 25
 LENGTH: 143
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS gene
 US-09-922-449B-25

Query Match 52.6%; Score 10; DB 12; Length 149;
 Best Local Similarity 52.6%; Pred. No. 5.1e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 31 CCAATTTCGGCTCCACG 49

RESULT 12

US-09-922-449B-10
 Sequence 10, Application US/09922449B
 Publication No. US20030148278A1
 GENERAL INFORMATION:
 APPLICANT: BioInside Gesellschaft fur Biodiagnostik, Auftragsforschung und Consulting mbH
 TITLE OF INVENTION: Test kit and method for quantitatively detecting genetically modified foodstuff by means of fluorescent-coupled PCR
 FILE REFERENCE: 101215-68
 CURRENT APPLICATION NUMBER: US/09/922,449B
 CURRENT FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: PCT/EP00/009835
 PRIOR FILING DATE: 2000-02-07
 NUMBER OF SEQ ID NOS: 8481

PRIOR APPLICATION NUMBER: DE 199 06 169.6
 PRIOR FILING DATE: 1999-02-08
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 10
 LENGTH: 150
 TYPE: DNA
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: reference IAC DNA for the RRS gene
 US-09-922-449B-10

Query Match 52.6%; Score 10; DB 12; Length 150;
 Best Local Similarity 52.6%; Pred. No. 5.1e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 32 CCAATTTCGGCTCCACG 50

RESULT 13

US-10-001-883-5/C
 Sequence 5, Application US/10001883
 Publication No. US20030022188A1
 GENERAL INFORMATION:
 APPLICANT: Macina, Roberto
 APPLICANT: Recipon, Herve
 APPLICANT: Plura, Jason
 APPLICANT: Chosch, Malavika
 APPLICANT: Sun, Yongming
 APPLICANT: Liu, Chenghua
 TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Their Expression
 FILE REFERENCE: DEX-0271
 CURRENT APPLICATION NUMBER: US/10/001,883
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/252,059
 PRIOR FILING DATE: 2000-11-20
 NUMBER OF SEQ ID NOS: 137
 SEQ ID NO: 5
 SOFTWARE: PatentIn version 3.1
 LENGTH: 167
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-001-883-5

Query Match 52.6%; Score 10; DB 14; Length 167;
 Best Local Similarity 52.6%; Pred. No. 5.2e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 CCAATNNNNNNNNCCACG 19
 Db 160 CCAATTGGAAATCACACG 142

RESULT 14

US-09-974-300-8096/C
 Sequence 8096, Application US/09974300
 Patent No. US2002014672A1
 GENERAL INFORMATION:
 APPLICANT: Berka, Randy M.
 APPLICANT: Clausen, Ib Groth
 TITLE OF INVENTION: Methods For Monitoring Multiple Gene Expression
 FILE REFERENCE: 10085-500-US
 CURRENT APPLICATION NUMBER: US/09/974,300
 CURRENT FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 09/680,598
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/279,526
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 8481

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8096
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1) ..(210)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-8096

Query Match      52.6%; Score 10; DB 10; Length 210;
Best Local Similarity 52.6%; Pred. No. 5.3e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy          1 CCAATNNNNNNNNCCACG 19
          ||||| | | | |
Db          152 CCAATTCTCGTCATCCACG 134

RESULT 15
US-09-778-320-59/c
Sequence 59, Application US/09778320
Patent No. US20010034052A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yiqiu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongrong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.491CS
CURRENT APPLICATION NUMBER: US/09/778,320
CURRENT PUBLISH DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 214
TYPE: DNA
ORGANISM: Homo sapien
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1) ..(214)
OTHER INFORMATION: n = A,T,C or G
US-09-778-320-59

Query Match      52.6%; Score 10; DB 9; Length 214;
Best Local Similarity 52.6%; Pred. No. 5.3e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy          1 CCAATNNNNNNNNCCACG 19
          ||||| | | | |
Db          88 CCAATTCTCATCTCCACG 70

Search completed: December 4, 2003, 08:51:36
Job time : 263 secs

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